

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 26, 2003, 08:34:37 ; Search time 67 Seconds

(without alignments)
984.464 Million cell updates/sec

Title: US-09-848-806-1

Perfect score: 2593

Sequence: 1 METKPNRRPSNTPLPYQTP.....KLNLFNIADAFVGDGKSD 495

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_101002.*

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23:	/SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2593	100.0	495	AA048000	Arabidopsis CDPK2
2	2458	94.8	501	AA035776	Arabidopsis thalia
3	2458	94.8	501	AA048001	Arabidopsis CDPK4
4	2064	79.6	425	AA035777	Arabidopsis thalia
5	1932	74.5	512	AA093256	Soybean CDPK prote
6	1924	74.2	399	AA035778	Arabidopsis thalia
7	1742	67.2	483	AA031158	Arabidopsis thalia
8	1742	67.2	556	AA031157	Arabidopsis thalia
9	1703	65.7	856	AA038599	Arabidopsis thalia
10	1703	65.7	893	AA038598	Arabidopsis thalia

11	1703	65.7	1017	21	AA038597	Arabidopsis thalia
12	1509.5	58.2	549	23	AA052842	Physcomitrella pat
13	1509	58.2	408	21	AA031159	Arabidopsis thalia
14	1501	57.9	463	21	AA046565	Arabidopsis thalia
15	1500	57.8	280	22	AA065758	ATCDPK2 kinase dom
16	1462	56.4	529	21	AA029590	Arabidopsis thalia
17	1462	56.4	542	21	AA029589	Arabidopsis thalia
18	1460.5	56.3	459	15	AA056237	Arabidopsis thalia
19	1457	56.2	569	15	AA056237	protein kinase spe
20	1325.5	51.1	538	21	AA043621	Arabidopsis thalia
21	1319	50.9	404	21	AA046566	Arabidopsis thalia
22	1231	47.5	378	21	AA046567	Arabidopsis thalia
23	1187.5	45.8	307	20	AA093255	Tobacco CDPK prote
24	1166.5	45.0	424	21	AA043622	Arabidopsis thalia
25	1153.5	44.5	421	21	AA043623	Arabidopsis thalia
26	1059	40.8	413	22	AA065755	ATCDPK kinase doma
27	1015.5	39.2	523	21	AA010101	Arabidopsis thalia
28	928.5	35.8	426	21	AA010102	Arabidopsis thalia
29	920.5	35.5	302	21	AA054428	zea mays protein f
30	900	34.7	274	22	AA065756	ATCDPK1 kinase dom
31	897	34.2	274	19	AA049837	Amino acid sequenc
32	887	34.2	274	22	AA065757	ATCDPK1A kinase do
33	887	34.2	274	22	AA065759	ATCDPK1A PK domain
34	849	32.7	597	23	AA052841	Physcomitrella pat
35	842.5	32.5	384	21	AA010103	Arabidopsis thalia
36	829	32.0	623	22	AA085583	Rice CDPK (clone r
37	771.5	29.8	456	16	AA074996	E. maxima Em70-1 a
38	753.5	29.1	504	21	AA016593	Arabidopsis thalia
39	753.5	29.1	594	21	AA016592	Arabidopsis thalia
40	737	28.4	502	21	AA053884	Arabidopsis thalia
41	737	28.4	594	21	AA053883	Arabidopsis thalia
42	712.5	27.5	428	21	AA016594	Arabidopsis thalia
43	712.5	27.5	524	21	AA018304	Plasmodium falci
44	694.5	26.8	189	23	AA059978	Human DITHP polype
45	690.5	26.6	414	21	AA053885	Arabidopsis thalia

ALIGNMENTS

RESULT 1
AA048000
ID AA048000 standard; Protein; 495 AA.

AC AA048000;

XX 08-MAR-2002 (first entry)

DT Arabidopsis CDPK2 SEQ ID NO 1.

DE Arabidopsis; CDPK2; CDPK4; calcium dependent protein kinase; oilseed;
KW disease resistance; agricultural; pathogen; crop yield; ornamental;
KW fungicide; bactericide; nematocide; insecticide; viricide; cereal;
KW transgenic; plant; enzyme.

XX Arabidopsis thaliana.

XX WO200184911-A1.

XX 15-NOV-2001.

XX 04-MAY-2001; 2001WO-US14368.

XX 05-MAY-2000; 2000US-201925P.

XX (GEO) GEN HOSPITAL CORP.

PI Sheen J;

DR WPI; 2002-062179/08.

XX N-PSDB; ABA06021.

PT Producing plant having increased disease resistance, comprises

PR	18-JUN-1999;	99US-0139458.
PR	18-JUN-1999;	99US-0139459.
PR	18-JUN-1999;	99US-0139460.
PR	18-JUN-1999;	99US-0139461.
PR	18-JUN-1999;	99US-0139462.
PR	18-JUN-1999;	99US-0139463.
PR	18-JUN-1999;	99US-0139750.
PR	18-JUN-1999;	99US-0139763.
PR	21-JUN-1999;	99US-0139817.
PR	22-JUN-1999;	99US-0139899.
PR	23-JUN-1999;	99US-0140353.
PR	23-JUN-1999;	99US-0140354.
PR	24-JUN-1999;	99US-0140695.
PR	28-JUN-1999;	99US-0140823.
PR	29-JUN-1999;	99US-0140991.
PR	30-JUN-1999;	99US-0141287.
PR	01-JUL-1999;	99US-0141842.
PR	01-JUL-1999;	99US-0142154.
PR	02-JUL-1999;	99US-0142055.
PR	06-JUL-1999;	99US-0142390.
PR	09-JUL-1999;	99US-0142920.
PR	12-JUL-1999;	99US-0142977.
PR	13-JUL-1999;	99US-0143542.
PR	14-JUL-1999;	99US-0143624.
PR	15-JUL-1999;	99US-0144005.
PR	16-JUL-1999;	99US-0144085.
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PR	23-JUL-1999;	99US-0145145.
PR	23-JUL-1999;	99US-0145218.
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PR	26-JUL-1999;	99US-0145276.
PR	27-JUL-1999;	99US-0145313.
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PR	27-JUL-1999;	99US-0145919.
PR	28-JUL-1999;	99US-0145951.
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PR	02-AUG-1999;	99US-0146388.
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Matches 470; Conservative 9; Mismatches 13; Indels 4; Gaps 1;		
QY	4	KPNPRPSNTVLPYQTPLRDRHYLLGKKGQGGTTLCTEKSTSNYACKSIPKPKLV 63
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Db	3	KPNPRPSNSVLPYETPLRDRHYLLGKKGQGGTTLCTEKSSSNYACKSIPKPKLV 62
		: : : : : : : :
QY	64	CREDYEDVWREIQIMHLSHPNVVRKGYEDSVFVHIVMEVCEGELFDRIYSKGHFS 123
		: : : : : : : :
Db	63	CREDYEDVWREIQIMHLSHPNVVRKGYEDSVFVHIVMEVCEGELFDRIYSKGHFS 122
		: : : : : : : :
QY	124	EREAVKLITLGVVEACHSILGVMHRLKPNFTLFDSPDKDAKLKATDFGLSVFKPGQY 183
		: : : : : : : :
Db	123	EREAVKLITLGVVEACHSILGVMHRLKPNFTLFDSPDDAKUKAIDFGLSVFKPGQY 182

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QY 184 LYDVVGSFYVAPVVKKCYGPEIDVWSAGVILYILLSGVPPFWAETESGIFRQILQGL 243
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DB 243 DFKSDPWTISEGAKDLIYKMLDRSPKKRISAHEALCHPWIVDHAAPDKPLDPAVLSRL 302
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DB 363 MESEIKSLMDAADINSCTIDYGEFLAATLHMNMKMERELIIVAFSDFDKDGGSYITIDE 422
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DB 423 LQACTEFGLCDTPLDDMIKEIDLNDGKIDFSEFTAMMKKGDGVRGSRRTMMKNLFNIA 482
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DB 483 EAFGVEDTSSTAKSD 498

RESULT 3
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AC AAM48001;
XX
DT 08-MAR-2002 (first entry)
DE Arabidopsis CDPK4 SEQ ID NO 3.
KW Arabidopsis; CDPK4; calcium dependent protein kinase; oilseed;
KW disease resistance; agricultural; pathogen; crop yield; ornamental;
KW fungicide; bactericide; nematocide; insecticide; viricide; cereal;
KW transgenic; plant; enzyme.
XX
OS Arabidopsis thaliana.
XX
XX WO200184911-A1.
XX
XX 15-NOV-2001.
XX
XX 04-MAY-2001; 2001WO-US14368.
XX
XX 05-MAY-2000; 2000US-201925P.
XX
XX (GCHO ) GEN HOSPITAL CORP.
XX
XX Sheen J;
XX
XX WPI; 2002-062179/08.
XX
XX N-PSDB; ABA06022.
XX
XX
XX Producing plant having increased disease resistance, comprises
XX regenerating plant from a non-naturally occurring plant cell
XX over-expressing a polynucleotide encoding a calcium dependent protein
XX kinase polypeptide -
XX
XX Disclosure; Fig 2; 44pp; English.
XX
XX The invention relates to producing a plant having increased disease
XX resistance, comprising providing a non-naturally occurring plant cell
XX over-expressing a polynucleotide encoding a calcium dependent protein
XX kinase (CDPK) polypeptide and regenerating a plant from the plant
XX cell, where the CDPK polypeptide is expressed in the plant, increasing
XX the resistance of the plant to disease as compared to a naturally
XX naturally-occurring plant. The method is useful for a variety of
XX agricultural and commercial purposes including improving a plant's
```

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CC resistance against plant pathogens, increasing crop yields, improving
CC crop and ornamental quality and reducing agricultural production costs.
CC the method facilitates an effective and economical method for in-plant
CC protection against plant pathogen, reducing or minimising the need for
CC traditional chemical practices (e.g, application of fungicides,
CC bactericides, nematocides, insecticides, or viricides) that are typically
CC used by farmers for controlling the spread of plant pathogens and
CC providing protection against disease causing pathogens. The method
CC contributes to the production of high quality and high yield agricultural
CC products, e.g. fruits, ornamentals, vegetables, cereals and field crops
CC having reduced spots, blemishes and blotches that are caused by
CC pathogens, agricultural products with increased shelf-life and reduced
CC handling costs and high quality and yield crops for agricultural
CC (e.g. cereal and field crops), industrial (e.g. oilseeds) and commercial
CC (e.g. fiber crops) purposes. The present sequence is that of Arabidopsis
CC thaliana CDPK4 of the invention.
XX
SQ Sequence 501 AA;
Query Match 94.8%; Score 2458; DB 23; Length 501;
Best Local Similarity 94.8%; Pred. No. 2.2e-210;
Matches 470; Conservative 9; Mismatches 13; Indels 4; Gaps 1;
QY 4 KPNRRPSNTVLPYQTPRLRDHYLLGKLGQGFQTTLYLCTEKSTSANYSACKSIPKRLV 63
DB 3 KPNRRPSNSVLPYETPRLRDHYLLGKLGQGFQTTLYLCTEKSSANYSACKSIPKRLV 62
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DB 63 CREDYEDVWREIQIMHJLSEHPNVVRIKGTYESDVFHVIMVEVCGGELFDRIVSKGCF 122
QY 124 EREAVKLITILGVVEACHSLGVMHRDLKPNELFDSKDDAKLKATDFGLSVFYKPGQY 183
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DB 183 LYDVVGSFYVAPVVKKCYGPEIDVWSAGVILYILLSGVPPFWAETESGIFRQILQGI 242
QY 244 DFKSDPWTISEAAKDLIYKMLERSPKKRISAHEALCHPWIVDQAPDKPLDPAVLSRL 303
DB 243 DFKSDPWTISEGAKDLIYKMLDRSPKKRISAHEALCHPWIVDHAAPDKPLDPAVLSRL 302
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QY 364 MESEIKSLMDAADINSCTIDYGEFLAATLHMNMKMERELIIVAFSDFDKDGGSYITIDE 423
DB 363 MESEIKSLMDAADINSCTIDYGEFLAATLHMNMKMERELIIVAFSDFDKDGGSYITIDE 422
QY 424 LQACTEFGLCDTPLDDMIKEIDLNDGKIDFSEFTAMMKKGDGVRGSRRTMMKNLFNIA 483
DB 423 LQACTEFGLCDTPLDDMIKEIDLNDGKIDFSEFTAMMKKGDGVRGSRRTMMKNLFNIA 482
QY 484 DAFGVDG----EKSD 495
DB 483 EAFGVEDTSSTAKSD 498

RESULT 4
ID AAG35777 standard; Protein; 425 AA.
XX
XX AAG35777;
XX
XX 18-OCT-2000 (first entry)
XX
XX Arabidopsis thaliana protein fragment SEQ ID NO: 43754.
XX
XX Protein identification; signal transduction pathway; metabolic pathway;
XX hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
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XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX XX
XX PD 06-SEP-2000.
XX XX
XX PF 25-FEB-2000; 2000EP-0301439.
XX XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
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PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
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PR 05-MAY-1999; 99US-0132484.
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PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
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PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

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Best Local Similarity 94.58; Pred. No. 2.4e-175;
Matches 399; Conservative 6; Mismatches 13; Indels 4; Gaps 1;

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Db 1 MHLSEHPNVVRIKGTEDSVFVHIVMEVCEGGELFDRIVSKGHFSEREAAKLKTIILGV 60

Qy 138 VEACHSLGVMRDLKPNFLFDSKDDAKLKATDFGLSVFYKPGQYLYDVVVGSPYYVAPE 197
Db 61 VEACHSLGVMRDLKPNFLFDSKDDAKLKATDFGLSVFYKPGQYLYDVVVGSPYYVAPE 120

Qy 198 VLKCYGPEIDVWAGVYLYLLSGVPPFWAETESGIFRQILQKGLDKPKDPWPTISEAA 257
Db 121 VLKCYGPEIDVWAGVYLYLLSGVPPFWAETESGIFRQILQKGLDKPKDPWPTISEGA 180

Qy 258 KDLIYKMLERSPKRISAEALCHPWIVDEQAAPDKPLDPAVLSRLKQFSOMNKKKNAAL 317
Db 181 KDLIYKMLDRSPKPKRISAEALCHPWIVDEHAAPDKPLDPAVLSRLKQFSOMNKKKNAAL 240

Qy 318 RVIARLSEEEIGGLKELFKMIDTNSGTITFEELKAGLRKRVGSELMSEIKSLMDAADI 377
Db 241 RVIARLSEEEIGGLKELFKMIDTNSGTITFEELKAGLRKRVGSELMSEIKSLMDAADI 300

Qy 378 DMSGIDYGEFLAATLHNMKEREELVAFSDKDGSGYITIDELQSACTEFLGCDTP 437
Db 301 DMSGIDYGEFLAATLHNMKEREELVAFSDKDGSGYITIDELQSACTEFLGCDTP 360

Qy 438 LDDMIKEIDLNDGKIDFSEFTAMMRKGDGVGRSRTMKNLNFNIADAFGVDBG----EKS 493
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Qy 494 DD 495
Db 421 DD 422

RESULT 5
AAW93256
ID AAW93256 standard; Protein; 512 AA.
XX AC AAW93256;
XX XX 25-AUG-1999 (first entry)
XX XX Soybean CDPK protein.
XX CDPK; calcium dependent protein kinase; tobacco; pathogen; invasion;
XX induction; elicitor; plant; disease resistance; parasiticein; soybean;
XX elicitin.
XX OS Glycine max.
XX XX
XX XX Location/Qualifiers
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XX FT /note= "protein kinase sequence"
XX FT Region 158..163
XX FT /note= "protein kinase sequence"
XX FT Region 198..205
XX FT /note= "protein kinase sequence"
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XX FT /note= "calcium binding site"
XX FT Binding-site 388..399
XX FT /note= "calcium binding site"
XX FT Binding-site 425..435
XX FT /note= "calcium binding site"
XX FT Binding-site 458..468
XX FT /note= "calcium binding site"
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XX XX WO9902655-A1.
XX XX 21-JAN-1999.
XX XX
XX PF 07-JUL-1998; 98WO-US14109.
XX XX
XX PR 08-JUL-1997; 97US-0889655.
XX XX
XX XX (KENT ) UNIV KENTUCKY RES FOUND.
XX XX
XX XX Chappell J, Lusso MFG;
XX XX
XX XX WPT; 1999-120859/10.
XX XX
XX XX New polynucleotides based on calcium dependent protein kinase genes
XX XX - useful to induce disease resistance in plants
XX XX
XX XX Example 4; Fig 4; 5lpp; English.
XX XX
XX CC This invention describes a novel nucleic acid molecule and its encoded
XX CC protein that are induced upon pathogen invasion or elicitor treatment.
XX CC The products of the invention are functional in plants, plant tissue and
XX CC in plant cells for inducible gene expression and altering the disease
XX CC resistance phenotype of plants. The products of the invention are
XX CC related to calcium dependent protein kinase (CDPK) genes. The invention
XX CC describes the isolation of a novel tobacco CDPK protein fragment and its
XX CC encoding nucleic acid, isolated from a cell suspension culture derived
XX CC from a tobacco cultivar KY14 explant, after growth in the presence of
XX CC the elicitor parasiticein. This sequence represents the soybean CDPK
XX CC protein which is used in the description of the method.
XX XX
XX XX Sequence 512 AA;
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PRECITY. 6

PR 21-JUL-1999; 99US-0144814.
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PR 29-OCT-1999; 99US-0162142.

Query Match 74.2%; Score 1924; DB 21; Length 399;
Best Local Similarity 94.2%; Pred. No. 6.7e-163;
Matches 373; Conservative 6; Mismatches 13; Indels 4; Gaps 1;

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Db 1 MEVCEGGELEFDRIVSKGCFSEAREAKLIKTLGVVACHSLGVVHMDLKPENFLFDPSPD 60

QY 164 DAKLKATDFGLSVFYKPGGYLYDVGVSPYVAPVVKCYGPEDVWSAGVILYILSGV 223
Db 61 DAKLKATDFGLSVFYKPGGYLYDVGVSPYVAPVVKCYGPEDVWSAGVILYILSGV 120

QY 224 PPFWAETESGIFRQILOGKLDKSDPWTISEAAKDLIYKMLERSPKKRISAHEALCHPW 283
Db 121 PPFWAETESGIFRQILOGKIDFKSDPWTISEGAKDLIYKMLDRSPKKRISAHEALCHPW 180

QY 284 IVDEQAAPDKPLDPVLSRLKQFSOMNKKKMAIRVIAERLSEEEIGGLKELFKMIDTGN 343
Db 181 IVDEHAAPDKPLDPVLSRLKQFSOMNKKKMAIRVIAERLSEEEIGGLKELFKMIDTGN 240

QY 344 SGTITFEELKAGLKVYGSSELMESEIKSLMDAADIDNSGTIDYGEFLAATLHNMKMEREEI 403
Db 241 SGTITFEELKAGLKVYGSSELMESEIKSLMDAADIDNSGTIDYGEFLAATLHNMKMEREEEN 300

QY 404 LVAAFSDFDKDGSYITIDELQSACTEFGCLDTPLDMMIKEIDLNDGKIDFSEFTAMMR 463
Db 301 LVVAFSYFDKDGSGYITIDELQQACTEFGCLDTPLDMMIKEIDLNDGKIDFSEFTAMMK 360

QY 464 KGDGVRGSRRTMMKNLNFNIADAFVGDG---EKSDD 495
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ID AAG31158 standard; Protein; 483 AA.
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AC AAG31158;
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DT 17-OCT-2000 (first entry)
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DE Arabidopsis thaliana protein fragment SEQ ID NO: 37372.
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
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OS Arabidopsis thaliana.
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PN EP1033405-A2.
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PF 25-FEB-2000; 2000EP-0301439.
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PR 23-AUG-1999; 99US-0149930.
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PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 67.2%; Score 1742; DB 21; Length 556;

Best Local Similarity 68.4%; Pred. No. 1.9e-146;

Matches 329; Conservative 56; Mismatches 84; Indels 2; Gaps 2;

QY 6 NRRPNTVLPYQTPRLRDHYLKGKIGQGQFGTTLCTEKSYSANYACKSIPKRLVCR 65

Db 77 NPDNQAYVVLGHKTPNIRDYITLSRKLGGQFGTTLCTEIASGVYACKSISKRKLISK 136

QY 66 EDYEDWRETOIMHLLSEHNVRKICTYEDSVFVHTVMEVCGGELFDRIVSKGHFSE 125

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PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
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PR 29-OCT-1999; 99US-0162142.

Query Match 65.7%; Score 1703; DB 21; Length 856;
Best Local Similarity 65.7%; Pred. No. 1e-142;
Matches 323; Conservative 64; Mismatches 81; Indels 24; Gaps 2;

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QY 50 ANYACKSIPKRLVCRDYEDVMREIOMHHLSEHPNPNVRIKGTYESDVHIVMEVCEG 109
DB 408 NEYACKSISKRLLTDEVEDVREIOMHHLAGHPNVISIKGAYEDVAVHIVMEICSG 467
QY 110 GELFDRTIVSKGFSEAEVKLIKITLGVBACHSLGVMHRDLKPENFLFDSPKDDAKLKA 169
DB 468 GELFDRIQGRHYTERKAAELARTIVGLEACHSLGVMHRDLKPENFLFVSREEDSLKT 527
QY 170 TDFGLSVFYKPGQYLDVVGSPYYVAPEVLKCYGPEIDVWSAGVILYLLSGVPPFWA- 228
DB 528 IDEGLSMFFKPEVFTDVVGSPYYVAPEVLKRYGPESDVWSAGVIVYLLSGVPPFWAG 587
QY 229 -----ETESGIFROILOGKLDKSDPWTITSEAAKDLIYKMLERSPKKRISAHE 277
DB 588 SEYNLFMSKYTEQTEQIFEQVLHGDLDFSSDPWPSISESAKDLVRKMLVDPKRLTAHQ 647
QY 278 ALCHPWIVDEQAAPKPLDPAVLRLKQFSQMNKIKKMLARVIAERLSEIEIGLKELFK 337
DB 648 VLCHPWVQIDGVAPDKPLDSAVLSRMKQFSAMNKKKMLARVIAESLSEIEIAGLKQMPK 707
QY 338 MIDTDSNGTTFPELKAGLRVSELMSEIKSLMDAADIDNSGTIDYGEFLAATLHMNK 397
DB 708 MIDADNSGQTFPEELKAGLRVGNLKESEILDIMQAADYDNGSTIDYKEFIATLHLNK 767
QY 398 MEREEIIVAAFSDFDKDGSVITIDELQSACTEFGLCDTPLDDMIKEIDLNDGKIDFSE 457
DB 768 IEREDHLFAAFSYFDKDESQIFTPDELOQACEEFGVEDARIEEMRMDVDQDKGRIDYNE 827
QY 458 FTAMMRKGDGVG 469
DB 828 FVAMMOKGSTMG 839

RESULT 10
AAG38598
ID AAG38598 standard; Protein; 893 AA.
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AC AAG38598;
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DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 47641.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EF1033405-A2.

XX PD 06-SEP-2000. 990S-0142055.
XX PF 06-JUL-1999; 990S-0142390.
XX PF 08-JUL-1999; 990S-0142803.
XX PF 09-JUL-1999; 990S-0142920.
XX PF 12-JUL-1999; 990S-0142977.
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PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 65.7%; Score 1703; DB 21; Length 893;
Best Local Similarity 65.7%; Pred. No. 1.1e-142;
Matches 323; Conservative 64; Mismatches 81; Indels 24; Gaps 2;

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QY 50 ANYACKSIPKRLVCRDIEDVREIQIMHLSHPNVRKIGTYEDSVFVHIWVEVCEG 109
D6 445 NEYACKSISKRKLLTDEVEDVREIQIMHLAGHPNVIKIGAYEDVAVHVMELCSG 504
QY 110 GELFDRIYSGHFSEREAVALIKITLGVWACHSLGVHMDLKPENFLFSPKDDAKLA 169
D6 505 GELFDRIIQRGHTERKAELARTIVGLACHSLGVHMDLKPENFLFVSREEDSLIKT 564
QY 170 TDFGLSVFYKPGGYLDVWGSPYYVAPEVLKCKYGPEDVMSAGVILYLLSGVPPFWA- 228
D6 565 IDFGLSMFFKPEDEFTDVWGSPYYVAPEVLKRYGPSDVMSAGVIVYLLSGVPPFWAG 624
QY 229 -----FTESGIFRILQGLKDFKSDPWPPTISEAKDLIYKMLERSPKKRISAHE 277
D6 625 SEVNLFSMKYTETEQGIFEQVLRHGLDLDVSSDPWPSISEAKDLVRLKMLRDPKRLTAHQ 684
QY 278 ALCHPWTVDQAAQDKPLDPVLSRLKQFSOMNKKIKKMLRVIAERLSEEBIGLKEFLK 337
D6 685 VLCHPWTVDQVADPKPLDSNVLRSKQFSAMNKKIKKMLRVIAERLSEEBIGLKEFLK 744
QY 338 MIDTNSGTITFEELKAGLRKVGSELMESEIKSLMDAADINSGTIDYGEFLAATLHMNK 397
D6 745 MIDADNSQITFEELKAGLRKVGANLKESEITLDMQAADVNSGTIDYKEFIATLHNLK 804
QY 398 MEREEILVAESDFDKGSGVITIDELQSACTEFGLCOTPLDDMIKELIDNDGKIDFSE 457
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DB 805 IEREDHLFAAFYFDKDESGFTTPELQOACEFVGVEDARIEEMMKDVEDODKDGRLDIYNE 864

QY 458 FTAMMRKGDGVG 469

DB 865 FVAMMOKGSGIMG 876

RESULT 11

AAG38597

ID AAG38597 standard; Protein; 1017 AA.

XX AAG38597;

DT 18-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 47640.

DE Protein identification; signal transduction pathway; metabolic pathway;

KW hybridisation assay; genetic mapping; gene expression control; promoter;

KW termination sequence.

XX Arabidopsis thaliana.

PN EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

PR 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.

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PR 29-OCT-1999; 99US-0162142.

Query Match 65.7%; Score 1703; DB 21; Length 1017;

Best Local Similarity 65.7%; Pred. No. 1.3e-142;

Matches 323; Conservative 64; Mismatches 81; Indels 24; Gaps 2;

QY 2 ETKPNRPP-----SNTVLPYQTPRLRDHYLLGKKLGGQGFQGTYYLCTEKSTS 49

DB 509 ETKBPQPKHMRVSSAGLRTESVLQRKTEFKBFYSLGRKLGGQGFQGTTFCLCKGTG 568

QY 50 ANYACKSPKRLKVCREDYEDVNRBIQIMHLSHPNVVRIKGTEDYSVFVHIVMEVCEG 109
DQ 569 NEYACKSISKRLLEDVEDVRETIQIMHLAGHPNVISIKGAYEDVAVHLMVMELCG 628
QY 110 GELFRIYVSGHFSREAVKILTKILGVVEACHSLGVHRLDKPENLDFSPKDDAKLKA 169
DQ 629 GELFRIIQRGHYTERKAELARTIVGLEACHSLGVHRLDKPENLDFVSEEDSLKT 688
QY 170 TDFGLSVFKPGQYLYDVGVSPYVAVPEYLKCYGPEIDVWSAGVILYLLSGVPFWA- 228
DQ 689 IDFGLSMEFKPDEVDTVVGVSPYVAVPEYLKRYGPESDVWSAGVILYLLSGVPFWAG 748
QY 229 -----ETESGIRFQILOGKLDKFDKDPWPTISERNAKDLIYKMLERSPKKLSAHE 277
DQ 749 SEVNLFSMKYITEQGIPEQVHLGDLDFSDPWPISSEAKDLVFKMLVDPKRLTAHQ 808
QY 278 ALCHPWIVDEQAAPKLPDPAVLSLKPSONKIKKMLRVIAERLSBEEITGLKELFK 337
DQ 809 VLCHPWVQIDGAPDKPLDPAVLSLKPSONKIKKMLRVIAERLSBEEITAGLKQMPK 868
QY 338 MIDTNSGTTITFEELKAGLKRYSSELSMESEIKSLMDAADIDNSGTIDYGEFTLAATHMKN 397
DQ 869 MIDADNSGTTITFEELKAGLKRYSSELSMESEIKSLMDAADIDNSGTIDYGEFTLAATHMKN 928
QY 398 MEREELIVAAFSDFKDGSGYITIDELQSACTEFGICLPTIDMDMIKEIDLNDGKIDFSE 457
DQ 929 IERDELFAAFSYFDKSGFTIDPELQQAEEFGEVDARIEEMRMVDQDKGRIDYNE 988
QY 458 FTAMMRKGDGVG 469
DQ 989 FVAMQKGSIMG 1000

RESULT 12
AAM52842

ID AAM52842 standard; Protein; 549 AA.

XX AAM52842;

22-FEB-2002 (first entry)

Physcomitrella patens CPK-2 protein, SEQ ID NO:39.

Protein kinase stress-related protein; PKSRP; moss; protein kinase-6;
PK-6; protein kinase-7; PK-7; protein kinase-8; PK-8; protein kinase-9;
PK-9; casein kinase homologue-1; CK-1; casein kinase homologue-2; CK-2;
casein kinase homologue-3; CK-3; mitogen-activated protein kinase;
MAP kinase-2; MPK-2; MAP kinase-3; MPK-3; MAP kinase-4; MPK-4;
MAP kinase-5; MPK-5; calcium-dependent protein kinase-1; CPK-1;
calcium-dependent protein kinase-2; CPK-2; overexpression;
environmental stress; salinity; drought; temperature; tolerance;
transgenic plant; EST; expressed sequence tag.

XX Physcomitrella patens.

OS WO2001177356-A2.

PN 18-OCT-2001.

XX 06-APR-2001; 2001WO-US11435.

PR 07-APR-2000; 2000US-196001P.

XX (BADI) BASF PLANT SCI GMBH.

PI Da Costa Silva EO, Bohnert HJ, Van Thiel N, Chen R;

PI Sarria-Millan R;

XX WPI; 2002-049153/06.

DR N-PSDB; ABA91081.

XX New protein, useful for increasing tolerance to environmental stress,
PT comprises a Protein Kinase Stress-Related Protein selected from

Protein kinases, Casein kinase homologs, MAP kinases or Calcium
dependent protein kinases -
PS Claim 13; Fig 3M; 154pp; English.

XX Sequences AAM52830-AAM52842 represent novel protein kinase stress-related
proteins (PKSRPs) from the moss Physcomitrella patens, and sequences
ABA91069-ABA91081 represent full-length cDNAs encoding them. The cDNA
sequences were obtained from expressed sequence tags (ESTs; ABA91056-
ABA91068) derived from Physcomitrella patens cDNA libraries. The PKSRPs
of the invention comprise protein kinase-6 (PK-6), protein kinase-7
(PK-7), protein kinase-8 (PK-8), protein kinase-9 (PK-9), casein kinase
homologue-1 (CK-1), casein kinase homologue-2 (CK-2), casein kinase
homologue-3 (CK-3), mitogen-activated protein (MAP) kinase-2 (MPK-2),
MAP kinase-3 (MPK-3), MAP kinase-4 (MPK-4), MAP kinase-5 (MPK-5),
calcium-dependent protein kinase-1 (CPK-1), and calcium-dependent protein
kinase-2 (CPK-2). When overexpressed, the PKSRPs are able to confer
tolerance to environmental stresses such as salinity, drought,
temperature, metal, chemical, pathogenic and oxidative stress.
Physcomitrella patens PKSRP nucleic acids may be used to generate
transgenic plants and seeds with increased tolerance to salinity, drought
and temperature. The transgenic plants generated can be monocots or
dicots and are especially maize, wheat, rye, oat, triticale, rice,
barley, cotton, rapeseed, cassava, sunflower, tagetes, leguminous plants
(e.g., soybean, peanut, vicia species, alfalfa), solanaceous plants
(e.g., potato, tobacco, aubergine, pepper, tomato), coffee, cacao, tea,
Salix species, oil palm, coconut, perennial grasses and forage crops. The
PKSRP nucleotide and proteins may also be used in evolutionary and
protein structural studies and as markers for specific regions of
the genome.

XX Sequence 549 AA;

Query Match 58.2%; Score 1509.5; DB 23; Length 549;
Best Local Similarity 60.8%; Pred. No. 9.9e-126;
Matches 290; Conservative 70; Mismatches 112; Indels 5; Gaps 3;

QY 5 PNPSPNT--VLPYQTPRLRDHLLGKLGQGGTLYLCTEKSTSNYACKSPKPK 61
DQ 69 PRPKPASVSGVLGKPLSDIRQSYILGRLGQGGTLYLCTEKSTSNYACKSPKPK 128
QY 62 LVCREDYEDVNRBIQIMHLSHPNVVRIKGTEDYSVFVHIVMEVCEGGEFDRIVSKGH 121
DQ 129 LYSKEDIEDVKREVQIMHLSGTPNIVLKDVFEDKSHVHLMVMELCAGGELFDRIAKGH 188
QY 122 FSEREAVKILTKILGVVEACHSLGVHRLDKPENLDFSPKDDAKLKDFTGLSVFKPG 181
DQ 189 YSERAADMCRIYVNVVHRCVSLGVHRLDKPENLDFSPKDDAKLKDFTGLSVFKPG 248
QY 182 QYLYDVGVSPYVAVPEYLKCYGPEIDVWSAGVILYLLSGVPFWAETESGIFRQLOG 241
DQ 249 DVFDIVGSAYVAVPEYLKCYGPEIDVWSAGVILYLLSGVPFWAETESGIFRQLOG 308
QY 242 KLDFKSDPWPPTISEAKDLIYKMLERSPKKLSAHEATLCHPWIVDEQAAPKLPDPAVLS 301
DQ 309 HIDFENDPWPPTISEAKDLIYKMLERSPKKLSAHEATLCHPWIVDEQAAPKLPDPAVLS 368
QY 302 RLKQFSQMNKIKKMLRVIAERLSBEEITGLKELFKMIDTNSGTITFEELKAGLKRYS 361
DQ 369 RLKQFSQMNKIKKMLRVIAERLSBEEITGLKELFKMIDTNSGTITFEELKAGLKRYS 428
QY 362 ELMESEIKSLMDAADIDNSGTIDYGEFTLAATHMKNMEREELIVAAFSDFKDGSGYIT 421
DQ 429 KLNESDIRKLEAADVGGKIDFNEFTSATMHNKTEKEDHLWAFMHFDNSGYIT 488
QY 422 DELQSACTEFGICLPTIDMDMIKEIDLNDGKIDFSEFTAMMRKGD-GVGRSRTMMK 476
DQ 489 DELQSACTEFGICLPTIDMDMIKEIDLNDGKIDFSEFTAMMRKGD-GVGRSRTMMK 545
RESULT 13
AAG31159
ID AAG31159 standard; Protein; 408 AA.

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AC AAG31159;
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XX 17-OCT-2000 (first entry)
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XX Arabidopsis thaliana protein fragment SEQ ID NO: 37373.
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XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
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XX Arabidopsis thaliana.
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XX 06-SEP-2000.
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PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match

57.98;

Score 1501; DB 21; Length 463;

Best Local Similarity

61.4%;

Pred. No. 4.4e-125;


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Matches 281; Conservative 79; Mismatches 92; Indels 6; Gaps 3;
QY 26 YILGKLGQGGTGYTLCTEKSTANYACKSIPKRLKVCREDYEDVWREIQIMHLSERP 85
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Db 8 YSLGELGRGQGVTHLCTQKATGHQFACKTIAKRLVKNKEDIEDVRREVQIMHLLTGGP 67
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 86 NVVRKIGTYEDSVFVHIVMEVCEGGELEFDRIYVSKGHFSEAEVAVKLKTLGVVEACHSLG 145
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 68 NIVELKGYEDKSHVHLMELCAGGELEFDRIIAKGHYSRAAASLLRTIVQIVHTCHSMG 127
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 146 VMHRDLKPNELFSDPKDAKLKATDFGLSVFYKPGQYLYDVVGSPPYVAPEVLKKCYGP 205
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 128 VIHROLKPNELLLNKDENSPLKATDFGLSVFYKPGVETKDIVGSAYIYAPEVLKRYGP 187
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 206 EIDVWSAGVILYLLSGVPPFWAETESGIFRQILQKLDPKSDPWTISEAAKDLIYKML 265
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 188 EADIWSIGVMLYLLCGVPPFWAETESGIFRQILQKLDPKSDPWTISEAAKDLIYKML 247
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 266 ERSPKRRISAHEALCHPWIVDQAAPOKPLDPAVLSRLKOFQSMNKKIKKMLRVIAERLS 325
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 248 NSDPQRLTAQAVLNHPWTKEDGEAPDVPDLNVAWSRLKOFKAMNFKKVALRVIAERLS 307
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 326 EEEIGLKLKFMIDTNSGTTIFELKAGLKRVSSEIEMSEIKSLMDAADTNSGTIDY 385
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 308 EEEIMGLKEMFKGMDTSSGTTILEELROGLAKQGTSLSEYEVQQLMEAADGNGTIDY 367
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 386 GEFLAATLHMKWEREILVAFFSDPKDGSYITIDELOSACTEFLGCD-TPLDMDIKE 444
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 368 GFETATMHNLDREELHYSFAFQHFQDKDNGSYITIMEELEQALREFGMNDGRDIKEIIS 427
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 445 IDLDNDGKIDSEFFAMRKG--DGVGRSRITMMKNLNF 480
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Db 428 VDGNDNGRINYDEFFVAMRKGNPDPIPKR---RELSEF 462
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RESULT 15
AAG65758
ID AAG65758 standard; Protein: 280 AA.
XX
AC AAG65758;
XX
XX 07-JAN-2002 (first entry)
DE ATCDPK2 kinase domain sequence.
KW Plant protoplast; gene expression; Arabidopsis; PK; CDPK; ATCDPK2;
KW calcium activated protein kinase; calcium dependant protein kinase.
XX
OS Arabidopsis thaliana.
XX
PN WO200168920-A1.
XX
PD 20-SEP-2001.
XX
PF 13-MAR-2001; 2001WO-US07999.
XX
PR 13-MAR-2000; 2000US-189074P.
XX
PA (GEMO ) GEN HOSPITAL CORP.
XX
PI Sheen J;
XX
DR WPI; 2001-611395/70.
XX
PT Using plant protoplast expression systems for rapidly screening
PT libraries of nucleic acids to identify gene that modulate expression of
PT target genes -
XX
PS Examples; Fig 3B; 95pp; English.
XX
CC The invention provides a high throughput assay for rapidly screening
CC a library of nucleic acid molecules to identify a gene product that
CC modulates expression of a gene of interest in plant protoplasts. The
```

```
method comprises: (1) introducing into 1 or more plant protoplasts:
CC (a) a reporter gene construct operably linked to a promoter of a gene of
CC interest; and (b) a member of a library of nucleic acid molecules (the
CC library member is expressed in the plant protoplasts); and (2) screening
CC the protoplasts to determine whether the amount of gene expression of the
CC reporter gene construct changes in response to the expression of the
CC library members, a change in gene expression of the reporter gene
CC construct identifying the gene product expressed by the library member as
CC 1 that modulates expression of the gene of interest. The present sequence
CC represents the amino acid sequence of Arabidopsis calcium dependant
CC protein kinase (CDPK) ATCDPK2 kinase domain.
XX
SQ Sequence 280 AA;
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Query Match 57.8%; Score 1500; DB 22; Length 280;
Best Local Similarity 100.0%; Pred. No. 2.6e-125;
Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 PSNTVLPYQTPRLRDHYLLGKLGKGGQFGCTTYLCTEKSTANYACKSIPKRLKVCREDYE 69
Db 1 PSNTVLPYQTPRLRDHYLLGKLGKGGQFGCTTYLCTEKSTANYACKSIPKRLKVCREDYE 60
QY 70 DVMREIQIMHLSSEHPNVVRIKGTIEDSVFVHIVMEVCEGGELEFDRIYVSKGHFSEAEVAVK 129
Db 61 DVMREIQIMHLSSEHPNVVRIKGTIEDSVFVHIVMEVCEGGELEFDRIYVSKGHFSEAEVAVK 120
QY 130 LKTLILGVVEACHSLGVHMRDLKPNFLDPSKDDAKLKATDFGLSVFYKPGQYLYDVVVG 189
Db 121 LKTLILGVVEACHSLGVHMRDLKPNFLDPSKDDAKLKATDFGLSVFYKPGQYLYDVVVG 180
QY 190 SPYYVAPEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETESGIFRQILQKLDPKSDP 249
Db 181 SPYYVAPEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETESGIFRQILQKLDPKSDP 240
QY 250 WPTISEAAKDLIYKMLERSPKKRISAHEALCHPWIVDEQA 289
Db 241 WPTISEAAKDLIYKMLERSPKKRISAHEALCHPWIVDEQA 280
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Search completed: March 26, 2003, 12:19:52
Job time : 72 secs

Result No.	Query %			DB	ID	Description
	Score	Match	Length			
1	1927	74.3	463	1	US-07-951-715A-25	Sequence 25, Appl
2	1927	74.3	463	2	US-08-459-448A-25	Sequence 25, Appl
3	1927	74.3	463	3	US-08-459-595A-25	Sequence 25, Appl
4	1927	74.3	463	3	US-08-459-504B-25	Sequence 25, Appl
5	1927	74.3	463	3	US-08-459-44A-25	Sequence 0, Appl
6	1927	74.3	463	4	US-09-547-422-25	Sequence 0, Appl
7	1672.5	64.5	639	4	US-09-347-801-17	Sequence 17, Appl
8	1437.5	55.4	464	1	US-07-951-715A-22	Sequence 22, Appl
9	1437.5	55.4	464	2	US-08-459-448A-22	Sequence 22, Appl
10	1437.5	55.4	464	3	US-08-459-595A-22	Sequence 22, Appl
11	1437.5	55.4	464	3	US-08-459-504B-22	Sequence 22, Appl
12	1437.5	55.4	464	3	US-08-459-44A-22	Sequence 0, Appl
13	1437.5	55.4	464	4	US-09-547-422-22	Sequence 0, Appl
14	1277.5	49.3	408	1	US-07-951-715A-21	Sequence 0, Appl
15	1277.5	49.3	408	2	US-08-459-448A-21	Sequence 21, Appl
16	1277.5	49.3	408	3	US-08-459-595A-21	Sequence 21, Appl
17	1277.5	49.3	408	3	US-08-459-504B-21	Sequence 21, Appl
18	1277.5	49.3	408	3	US-08-459-44A-21	Sequence 21, Appl
19	1277.5	49.3	408	4	US-09-547-422-21	Sequence 21, Appl
20	829	32.0	623	4	US-09-347-801-4	Sequence 4, Appl
21	826	31.9	625	4	US-09-347-801-18	Sequence 18, Appl
22	800	30.9	576	4	US-09-347-801-19	Sequence 19, Appl
23	771.5	29.8	456	1	US-08-464-164-2	Sequence 2, Appl
24	771.5	29.8	456	1	US-08-338-057-2	Sequence 2, Appl
25	771.5	29.8	456	2	US-08-668-416-2	Sequence 2, Appl
26	622	24.0	520	4	US-09-257-825B-20	Sequence 20, Appl
27	567.5	22.7	370	2	US-08-878-98B-19	Sequence 19, Appl

INFORMATION FOR SEQ ID NO: 25;
SEQUENCE CHARACTERISTICS:
LENGTH: 463 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: Protein
LOCATION: 1..463
OTHER INFORMATION: /note= "protein sequence for
OTHER INFORMATION: soybean CDPK as shown in Figure 34."
US-07-951-715A-25

Query Match 74.3%; Score 1927; DB 1; Length 463;
Best Local Similarity 78.7%; Pred. No. 1e-152;
Matches 365; Conservative 49; Mismatches 48; Indels 2; Gaps 2;
QY 14 VLPQTPRLRDLHLLGKLGQGFQGTITLCTEKSSTANYACKSIPKRLVCREDEDYVWR 73
DB 1 VLPQTONIREVYEVGRKLGQGFQGTITCTRRASGGKFAKSIPIKRLCKEDYVWR 60
QY 74 EIQIMHLSHPNVVRIKGTEDSVFVHVMVCEGGLFDRIVSKGHFSEREAVKLTK 133
DB 61 EIQIMHLSHANVVRIGETEDSTAVHLVMECEGGLFDRIVQKGYHSEQAARLTK 120
QY 134 ILGVVEACHSLGVMDLKPENFLPDSKDDAKLTKATDGLSVFYKPGQYLDVVGSPY 193
DB 121 IVEVVEACHSLGVMDLKPENFLDTIDEDAKLTKATDGLSVFYKPGESFCDDVVGSPY 180
QY 194 VAPEVLKCYGPEIDVWSAGVILYILLSGVPPFWAETSGIFRQILQKLDKSPDPWPTI 253
DB 181 VAPEVLKLYGPEIDVWSAGVILYILLSGVPPFWAETSGIFRQILQKLDKSPDPWPTI 240
QY 254 SPAADLIYKMLERSPKKRISAEALCHPWIVDEQAADPKLPDPAVLSRLKQFSOMNLIK 313
DB 241 SDSAKDLIRKMLDQNPKTRLTAHEVLRHPWIVDDNIAPDKPDSAVLSRLKQFSAMNLIK 300
QY 314 KNALRVIAERLSEEBEIGGLKELFKMIDTNSGTITFEELKAGLKRVSGLMESEIKSLMD 373
DB 301 KNALRVIAERLSEEBEIGGLKELFKMIDTNSGTITFEELKAGLKRVSGLMESEIKSLMD 360
QY 374 AADINSGTIDYGEFLATLHNKKWEREILVAASDFDKGSGYITIDELASACTEFL 433
DB 361 AADIDKSGTIDYGEFLATLHNKKWEREILVAASDFDKGSGYITIDELASACTEFL 420
QY 434 CDTPLDDMIKEDLDNDGKIDSEFTAMMRKGD-GVGRSRTMMK 476
DB 421 DDHIDDDMIKEDLDNDGQIDYGEFTAMMRKGGIGR-RTMRK 463

RESULT 2
US-08-459-448A-25
Sequence 25, Application US/08459448A
Patent No. 5859336
GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
APPLICANT: Desai, Nalini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Lannis, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.

TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: NO. 5859336artis Corporation
STREET: Patent & Trademark Dept., 520 White Plains
STREET: Rd., POB 2005
CITY: Tarrytown
STATE: New York
COUNTRY: USA
ZIP: 10591-9005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,448A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: 40403
REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8582
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 463 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: Protein
LOCATION: 1..463
OTHER INFORMATION: /note= "protein sequence for
OTHER INFORMATION: soybean CDPK as shown in Figure 34."
US-08-459-448A-25

Query Match 74.3%; Score 1927; DB 2; Length 463;
Best Local Similarity 78.7%; Pred. No. 1e-152;
Matches 365; Conservative 49; Mismatches 48; Indels 2; Gaps 2;
QY 14 VLPQTPRLRDLHLLGKLGQGFQGTITLCTEKSSTANYACKSIPKRLVCREDEDYVWR 73
DB 1 VLPQTONIREVYEVGRKLGQGFQGTITCTRRASGGKFAKSIPIKRLCKEDYVWR 60
QY 74 EIQIMHLSHPNVVRIKGTEDSVFVHVMVCEGGLFDRIVSKGHFSEREAVKLTK 133
DB 61 EIQIMHLSHANVVRIGETEDSTAVHLVMECEGGLFDRIVQKGYHSEQAARLTK 120
QY 134 ILGVVEACHSLGVMDLKPENFLPDSKDDAKLTKATDGLSVFYKPGQYLDVVGSPY 193
DB 121 IVEVVEACHSLGVMDLKPENFLDTIDEDAKLTKATDGLSVFYKPGESFCDDVVGSPY 180
QY 194 VAPEVLKCYGPEIDVWSAGVILYILLSGVPPFWAETSGIFRQILQKLDKSPDPWPTI 253
DB 181 VAPEVLKLYGPEIDVWSAGVILYILLSGVPPFWAETSGIFRQILQKLDKSPDPWPTI 240
QY 254 SPAADLIYKMLERSPKKRISAEALCHPWIVDEQAADPKLPDPAVLSRLKQFSOMNLIK 313
DB 241 SDSAKDLIRKMLDQNPKTRLTAHEVLRHPWIVDDNIAPDKPDSAVLSRLKQFSAMNLIK 300
QY 314 KNALRVIAERLSEEBEIGGLKELFKMIDTNSGTITFEELKAGLKRVSGLMESEIKSLMD 373

Db 301 KMALRVIAERLSEEEIGGLKELFKMIDTNSGTTITFDELKQGLKRVGSELMESEIKDLMD 360
QY 374 AADIDNSGTIDYGEFLAATLHMKNKMEREEILVAAFSDFDKDGSGYITIDELQSACTEFG 433
Db 361 AADIDKSGTIDYGEFLAATVHLKLERENLYSAFSYFDKDGSGYITIDELQOACKDFGL 420
QY 434 CDTPLDDMIKEIDLNDGKIDFSEFTAMMRKGD-GVGRSRTMMK 476
Db 421 DDHIDDMIKEDQNDGQIDYGEFAAMMRKGGGIGR-RTMRK 463

RESULT 3
US-08-459-595A-25
; Sequence 25, Application US/08459595A
; Patent No. 6018104
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6018104artis Corporation
; STREET: Patent & Trademark Dept., 520 White Plains
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591-9005

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,595A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Gary M.
; REGISTRATION NUMBER: 40403
; REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8582
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 463 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..463
; OTHER INFORMATION: /note= "protein sequence for
; OTHER INFORMATION: soybean CDPK as shown in Figure 34."
US-08-459-595A-25
Query Match 74.3%; Score 1927; DB 3; Length 463;
Best Local Similarity 78.7%; Pred. No. 1e-152;
Matches 365; Conservative 49; Mismatches 48; Indels 2; Gaps 2;
QY 14 VLPYOTPRLRDHYLLGKLGQOGFTTYLCTEKSISANYACKSIKPKLVCREDEYDVR 73
Db 1 VLPQRTQNTIREYVEYGRKLGQOGFTTETTRASGGKFAKSIKPKLLCKEDYDVR 60
QY 74 EIQIMHLSHPNVVRIKGTEDSVFVHTVMVEVCGGELFDRIVSKGFHSEAEVKKLKT 133
Db 61 EIQIMHLSHPNVVRIKGTEDSVFVHTVMVEVCGGELFDRIVSKGFHSEAEVKKLKT 120
QY 134 ILGVVEACHSLGVHRLDKPENFLFSDSPKDDAKLKATDFGLSVFYKPGQYLYDVVGSPPY 193
Db 121 IVEVVEACHSLGVHRLDKPENFLFDTTDEDAKLKATDFGLSVFYKPGESFCDVVGSPPY 180
QY 194 VAPEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETSGIFRQILQGLDKSPDPWPTI 253
Db 181 VAPEVLRKLYGPESDVWSAGVILYLLSGVPPFWAETSGIFRQILQGLDKSPDPWPTI 240
QY 254 SEAAKDLVYKMLERSPKKRISAHREALCHPWIVDEQAAAPKPLDPAVLSRLKQFSOMNKK 313
Db 241 SDSAKDLIRKMLQDPKPKRLTAHEVRHPWIVDDIADPKLDSAVLSRLKQFSOMNKK 300
QY 314 KMALRVIAERLSEEEIGGLKELFKMIDTNSGTTITFDELKQGLKRVGSELMESEIKSLMD 373
Db 301 KMALRVIAERLSEEEIGGLKELFKMIDTNSGTTITFDELKQGLKRVGSELMESEIKDLMD 360
QY 374 AADIDNSGTIDYGEFLAATLHMKNKMEREEILVAAFSDFDKDGSGYITIDELQSACTEFG 433
Db 361 AADIDKSGTIDYGEFLAATVHLKLERENLYSAFSYFDKDGSGYITIDELQOACKDFGL 420
QY 434 CDTPLDDMIKEIDLNDGKIDFSEFTAMMRKGD-GVGRSRTMMK 476
Db 421 DDHIDDMIKEDQNDGQIDYGEFAAMMRKGGGIGR-RTMRK 463

RESULT 4
US-08-459-504B-25
; Sequence 25, Application US/08459504B
; Patent No. 6075185
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6075185artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park

```
? STATE: NC
? COUNTRY: USA
? ZIP: 27709
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/459,504B
? FILING DATE:
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/459,595
? FILING DATE: 02-JUN-1995
? APPLICATION NUMBER: US 07/951,715
? FILING DATE: 25-SEP-1992
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/772,027
? FILING DATE: 04-OCT-1991
? ATTORNEY/AGENT INFORMATION:
? NAME: Meigs, J. Timothy
? REGISTRATION NUMBER: 38,241
? REFERENCE/DOCKET NUMBER: CGC1577/CIP/DIV
? TELEPHONE: (919)541-8587
? TELEFAX: (919)541-8689
? INFORMATION FOR SEQ ID NO: 25:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 463 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? HYPOTHETICAL: NO
? FEATURE:
? NAME/KEY: Protein
? LOCATION: 1..463
? OTHER INFORMATION: /note= "protein sequence for
? soybean CDPK as shown in Figure 34."
US-08-459-504B-25

Query Match 74.3%; Score 1927; DB 3; Length 463;
Best Local Similarity 78.7%; Pred. No. 1e-152;
Matches 365; Conservative 49; Mismatches 48; Indels 2; Gaps 2;

Qy 14 VLPQTPLRDLHYLLGKKGQGGFTTYLCTEKSTSANYSACKSPKRLKVCREDYEDVWR 73
Db 1 VLPQTQIRVEYEVGRKLGQGGFTTTECTRRASGGKFAKSPKRLKCKEDYEDVWR 60

Qy 74 EIQIMHLSHPNVVRKIGTYEDSVFVHVMVCEGGELFDRIVSKGHFSREAVKLTKT 133
Db 61 EIQIMHLSHANVVRIGTYEDSTAVHLVMELCGGELFDRIVKQGHYSERQARLTKT 120

Qy 134 ILGVVEACHSLGVMRDLKPNFLDPSKDDAKLKATDFGLSVFYKPGQYLYDVVGSPPY 193
Db 121 IVEVVEACHSLGVMRDLKPNFLDTTDEDAKLKATDFGLSVFYKPGSECDVVGSPY 180

Qy 194 VAPEVLKCYGPEIDVNSAGVILYLLSGVPPFNAETSGIFRQILQKLDKFPKDPWPTI 253
Db 181 VAPEVLRLKLYGPESDVSAGVILYLLSGVPPFNAETSGIFRQILKGLDFHSEPPWPSI 240

Qy 254 SEAAKDLVKKLERSPKKRISAEALCPWIVDEQAAPDKPLDPVLSRLKQFSOMNKK 313
Db 241 SDSAKDLIRKMLDQPKTRFLTAHEVLRHPWIVDDNIAPDKPLDSAVLSRLKQFSAMNKK 300

Qy 314 KMLRVIAERLSEEEIGGLKELFKMIDTNSGTITFEELKAGLRVSGELMESETKSLMD 373
Db 301 KMLRVIAERLSEEEIGGLKELFKMIDTNSGTITFDELKGLKRVSGELMESETKSLMD 360

Qy 374 AADINDSGTIDYGEFLAATLHMNMKEEELVAAFSDFDKDGSYITIDELQSACTEGL 433
Db 361 AADIDKSGTIDYGEFTAATVHLNKEENLVSAFSDYFDKDGSGYITIDELQQAACKDRGL 420

Qy 434 CDTPLDDMIKELDLDNGKIDSEFTAMMRKGD-GVGRSRTMMK 476
Db 421 DDIIHDDMIKELDQNDQIDYGEFAAMMRKGGIGR-RTMRK 463

RESULT 5
US-08-459-444-25
? Sequence 0, Application US/08459444A
? Patent No. 6121014
? GENERAL INFORMATION:
? APPLICANT: Koziel, Michael G.
? Desai, Nallini M.
? Lewis, Kelly S.
? Kramer, Vance C.
? Warren, Gregory W.
? Evola, Stephen V.
? Crossland, Lyle D.
? Wright, Martha S.
? Merlin, Ellis J.
? Launis, Karen L.
? TITLE OF INVENTION: METHOD FOR PRODUCING A PLANT-OPTIMIZED
? NUCLEIC ACID CODING SEQUENCE
? NUMBER OF SEQUENCES: 94
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: No. 6121014artis Agribusiness Biotechnology Research, Inc.
? STREET: 3054 Cordwallis Road
? CITY: Research Triangle Park
? STATE: NC
? COUNTRY: USA
? ZIP: 27709
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/459,444A
? FILING DATE: 02-Jun-1995
? CLASSIFICATION: <Unknown>
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/951,715
? FILING DATE: 25-SEP-1992
? APPLICATION NUMBER: US 07/772,027
? FILING DATE: 04-OCT-1991
? ATTORNEY/AGENT INFORMATION:
? NAME: Meigs, J. Timothy
? REGISTRATION NUMBER: 38,241
? REFERENCE/DOCKET NUMBER: S-18805/P1/CGC1577/CIP/DIV6
? TELEPHONE: (919)541-8587
? TELEFAX: (919)541-8689
? INFORMATION FOR SEQ ID NO: /note= "protein sequence for
? soybean CDPK as shown in Figure 34."
US-08-459-444-25

Query Match 74.3%; Score 1927; DB 3; Length 463;
Best Local Similarity 78.7%; Pred. No. 1e-152;
Matches 365; Conservative 49; Mismatches 48; Indels 2; Gaps 2;

Qy 14 VLPQTPLRDLHYLLGKKGQGGFTTYLCTEKSTSANYSACKSPKRLKVCREDYEDVWR 73
Db 1 VLPQTQIRVEYEVGRKLGQGGFTTTECTRRASGGKFAKSPKRLKCKEDYEDVWR 60

Qy 74 EIQIMHLSHPNVVRKIGTYEDSVFVHVMVCEGGELFDRIVSKGHFSREAVKLTKT 133
Db 61 EIQIMHLSHANVVRIGTYEDSTAVHLVMELCGGELFDRIVKQGHYSERQARLTKT 120

Qy 134 ILGVVEACHSLGVMRDLKPNFLDPSKDDAKLKATDFGLSVFYKPGQYLYDVVGSPPY 193
Db 121 IVEVVEACHSLGVMRDLKPNFLDTTDEDAKLKATDFGLSVFYKPGSECDVVGSPY 180

Qy 194 VAPEVLKCYGPEIDVNSAGVILYLLSGVPPFNAETSGIFRQILQKLDKFPKDPWPTI 253
Db 181 VAPEVLRLKLYGPESDVSAGVILYLLSGVPPFNAETSGIFRQILKGLDFHSEPPWPSI 240

Qy 254 SEAAKDLVKKLERSPKKRISAEALCPWIVDEQAAPDKPLDPVLSRLKQFSOMNKK 313
Db 241 SDSAKDLIRKMLDQPKTRFLTAHEVLRHPWIVDDNIAPDKPLDSAVLSRLKQFSAMNKK 300

Qy 314 KMLRVIAERLSEEEIGGLKELFKMIDTNSGTITFEELKAGLRVSGELMESETKSLMD 373
Db 301 KMLRVIAERLSEEEIGGLKELFKMIDTNSGTITFDELKGLKRVSGELMESETKSLMD 360

Qy 374 AADINDSGTIDYGEFLAATLHMNMKEEELVAAFSDFDKDGSYITIDELQSACTEGL 433
Db 361 AADIDKSGTIDYGEFTAATVHLNKEENLVSAFSDYFDKDGSGYITIDELQQAACKDRGL 420
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Db 1 VLPQNTQIRVYEVGRKLGQGGQGTFFECTRRASGGKFAKSPKRLKCKEDYEDVWR 60
QY 74 EIQIMHHLSEHPNVVRIKGTEDSVFVHVMVECGEGELFDRIYVSKGHFSREAVKLIKT 133
Db 61 EIQIMHHLSEHPNVVRIKGTEDSVFVHVMVECGEGELFDRIYVSKGHFSREAVKLIKT 120
QY 134 ILGVVEACHSLGVHMDLKPENFLDSDPAKLAATDGLSVFYKPGQYLYDVVGSPPY 193
Db 121 IVEVVEACHSLGVHMDLKPENFLDSDPAKLAATDGLSVFYKPGQYLYDVVGSPPY 180
QY 194 VAPEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETSGIFRQLQGLKDFKSDPWTI 253
Db 161 VAPEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETSGIFRQLQGLKDFKSDPWTI 240
QY 254 SEAKDLIYKMLERSPKKRISAEALCHPWIVDEQAAPDKPLDPAVLSRLKQFSOMNLIK 313
Db 241 SDSAKDLIRKMLDQNPRTLAHEVLRHPWIVDDNIAPDKPLDPAVLSRLKQFSOMNLIK 300
QY 314 KMLRVIAERLSEEEIGGLKELFKMIDTNSGTITTFEELKAGLRKVGSELMESEIKSLMD 373
Db 301 KMLRVIAERLSEEEIGGLKELFKMIDTNSGTITTFEELKAGLRKVGSELMESEIKSLMD 360
QY 374 AADIDNSGTIDYGEFLAATLHNMKMERBEILVAAFSDFDKDGSGYITIDELQSACTEFL 433
Db 361 AADIDNSGTIDYGEFLAATLHNMKMERBEILVAAFSDFDKDGSGYITIDELQSACTEFL 420
QY 434 CDTPLDDMIKEIDLDNGKIDFSEFTAMMRKGD-GVGRSRTMMK 476
Db 421 DDHIDDDMIKEIDLDNGKIDFSEFTAMMRKGD-GVGRSRTMMK 463

RESULT 6

US-09-547-422-25

; Sequence 0, Application US/09547422
; Patent No. 6320100
; GENERAL INFORMATION:

APPLICANT: Koziel, Michael G.

Desai, Nallini M.

Lewis, Kelly S.

Kramer, Vance C.

Warren, Gregory W.

Evola, Stephen V.

Crossland, Lyle D.

Wright, Martha S.

Merlin, Ellis J.

Launis, Karen L.

TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED

INSECTICIDAL ACTIVITY IN MAIZE

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESS: No. 6320100artis Agribusiness Biotechnology Research, Inc.

STREET: 3054 Cornwallis Road

CITY: Research Triangle Park

STATE: NC

COUNTRY: USA

ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/547,422

FILING DATE: 11-Apr-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/459,595

FILING DATE: 02-JUN-1995

APPLICATION NUMBER: US 07/951,715

FILING DATE: 25-SEP-1992

APPLICATION NUMBER: US 07/772,027

FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:

; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: S-18805H
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8587
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: /note= "protein sequence for
; soybean CDPK as shown in Figure 34."
; SEQUENCE CHARACTERISTICS:
; LENGTH: 463 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..463
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-547-422-25

Query Match

Best Local Similarity 74.3%; Score 1927; DB 4; Length 463;

Matches 365; Conservative 49; Mismatches 48; Indels 2; Gaps 2;

QY 14 VLPQNTQIRVYEVGRKLGQGGQGTFFECTRRASGGKFAKSPKRLKCKEDYEDVWR 73
Db 1 VLPQNTQIRVYEVGRKLGQGGQGTFFECTRRASGGKFAKSPKRLKCKEDYEDVWR 60
QY 74 EIQIMHHLSEHPNVVRIKGTEDSVFVHVMVECGEGELFDRIYVSKGHFSREAVKLIKT 133
Db 61 EIQIMHHLSEHPNVVRIKGTEDSVFVHVMVECGEGELFDRIYVSKGHFSREAVKLIKT 120
QY 134 ILGVVEACHSLGVHMDLKPENFLDSDPAKLAATDGLSVFYKPGQYLYDVVGSPPY 193
Db 121 IVEVVEACHSLGVHMDLKPENFLDSDPAKLAATDGLSVFYKPGQYLYDVVGSPPY 180
QY 194 VAPEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETSGIFRQLQGLKDFKSDPWTI 253
Db 161 VAPEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETSGIFRQLQGLKDFKSDPWTI 240
QY 254 SEAKDLIYKMLERSPKKRISAEALCHPWIVDEQAAPDKPLDPAVLSRLKQFSOMNLIK 313
Db 241 SDSAKDLIRKMLDQNPRTLAHEVLRHPWIVDDNIAPDKPLDPAVLSRLKQFSOMNLIK 300
QY 314 KMLRVIAERLSEEEIGGLKELFKMIDTNSGTITTFEELKAGLRKVGSELMESEIKSLMD 373
Db 301 KMLRVIAERLSEEEIGGLKELFKMIDTNSGTITTFEELKAGLRKVGSELMESEIKSLMD 360
QY 374 AADIDNSGTIDYGEFLAATLHNMKMERBEILVAAFSDFDKDGSGYITIDELQSACTEFL 433
Db 361 AADIDNSGTIDYGEFLAATLHNMKMERBEILVAAFSDFDKDGSGYITIDELQSACTEFL 420
QY 434 CDTPLDDMIKEIDLDNGKIDFSEFTAMMRKGD-GVGRSRTMMK 476
Db 421 DDHIDDDMIKEIDLDNGKIDFSEFTAMMRKGD-GVGRSRTMMK 463

RESULT 7

US-09-347-801-17

; Sequence 17, Application US/09347801

; Patent No. 6262345

; GENERAL INFORMATION:

APPLICANT: Allen, Steve

APPLICANT: Lee, Jian Ming

TITLE OF INVENTION: Plant Protein Kinases

FILE REFERENCE: BB-1171

CURRENT APPLICATION NUMBER: US/09/347,801

CURRENT FILING DATE: 1999-07-02

EARLIER APPLICATION NUMBER: 60/092,438

EARLIER FILING DATE: July 10, 1998

NUMBER OF SEQ ID NOS: 23

SOFTWARE: Microsoft Office 97

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; SEQ ID NO 17
; LENGTH: 639
; TYPE: PRT
; ORGANISM: Zea mays
; US-09-347-801-17

Query Match          64.5%; Score 1672.5; DB 4; Length 639;
Best Local Similarity 66.2%; Pred. No. 2.6e-131;
Matches 318; Conservative 66; Mismatches 83; Indels 13; Gaps 3;

QY 5 PNPR-RPS-----NTVLPYQPRLRDHYLLGKLGQGGFGTGYLTCTKSTKSANY 52
Db 120 PSPPRPQVKKRVSSAGLLGSLVLRKKTENLKDKYSLGRLLGQGGFGTGLCVERATGKEL 179
QY 53 AKSIPKRLVCRDYEVDVREIQIMHLSHPNNVRIKGTYESVPHVMEVCEGDEL 112
Db 180 ACKSILKRLGSDDDVEDVREIQIMHLSHAGHPSVVGIRGAYEDAVAVHLMELCGGDEL 239
QY 113 FDRIVSGHFSEREAVKLITILGWVACHSLGVMHRLKPNFLDPSKDDAKLKATDF 172
Db 240 FDRIVRGHTTERKAELARVIVGVVACHSGVMHRLKPNFLDADHSEEAALKTIIDF 299
QY 173 GLSVFYKPGQYLDVVGSPYYVAPEVLKCYGPEIDVMSAGVILYLLSGVPPFWAETES 232
Db 300 GLSIFRPGQIFTDVVGSPYYVAPEVLKRYGPEADVMSAGVILYLLSGVPPFWAENQ 359
QY 233 GIFQILOGKLDKSDPWPPISEAAKOLIVKMLERSPKKRLISAHEALCHPWIVDEQAPD 292
Db 360 GIFBEVLHGRIDFSESPWPSISDGAOKDLVRRMLVRDPKRLTAHEVLRHPVWQGVGAPD 419
QY 293 KPLDPVAVLSRLKQPSOMNKKKMLRALYIAERLSPEEIGGLKELFKMTDTONSGTITPEEL 352
Db 420 RPLDSAVLSRMKQPSAMNKKKMLRALYIAENLSEDETAGLREMEKMDADNSGOITPEEL 479
QY 353 KAGLKRVSLEMESEIKSLMDAADINSGTIDYGEFTLAATHLMKMEREEILYVAAFSDFD 412
Db 480 KVGLEKYGANLQSEIYALMQAADVNDNGTIDYGEFTLAATHLMKMEREDHLFAAFQVFD 539
QY 413 KDGSGYITIDBLQSACTEFGLCDPLDDMIKEIDLDNDGKIDFSEFTAMMKDGVGGRSR 472
Db 540 KDGSGYITADELVQACEFGLGDVQLEDLGEVDQDNDGRIDYNEFFVAMMKQ-PTVGGSR 598

RESULT 8
us-07-951-715A-22
; Sequence 22, Application US/07951715A
; Patent No. 5625136
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
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; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/951,715A
; FILING DATE: 25-SEP-1992
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Spruill, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8615
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 464 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..464
; OTHER INFORMATION: /note= "derived protein sequence of
; OTHER INFORMATION: pollen specific CDPK as disclosed in Figure 34."
; US-07-951-715A-22

Query Match          55.4%; Score 1437.5; DB 1; Length 464;
Best Local Similarity 60.9%; Pred. No. 6.7e-112;
Matches 271; Conservative 70; Mismatches 103; Indels 1; Gaps 1;

QY 22 LRDHVLLGKLGQGGFGTGYLTCTKSTKSANYACKSIPKRLVCRDYEVDVREIQIMHHL 81
Db 9 VRAVYSMGLKGRGQGVTHLCTHRTSGEKLACKTIARKLAAHEDVDVRRVREIQIMHHL 68
QY 82 SEHPNVVRIKGTYESVPHVMEVCEGDELFDRIIVSKGHFSEREAVKLITILGVVEAC 141
Db 69 SCQPNVVGRCAYEDKQSVHVMELCAGGELFDRLIARGQYTERGAELLRAIVQIVHTC 128
QY 142 HSLGVHMRDLKPNFLDPSKDDAKLKATDPGLSVFYKPGQYLDVVGSPYYVAPEVLK 201
Db 129 HSMGVHMRDLKPNFLDPSKDDAKLKATDPGLSVFYKPGQYLDVVGSPYYVAPEVLK 188
QY 202 CYGPEIDVMSAGVILYLLSGVPPFWAETESGIFRQILOGKLDKFDKSDPWPPISEAAKDLI 261
Db 189 KYGPEADIVSGVWLYIFLAGVPPFWAENSGIITAILRGQDLSSSEPPWHPISGAKDLV 248
QY 262 YKMLERSPKKRLISAHEALCHPWIVDEQAPDKPLDPAVLSRLKQPSOMNKKKMLRALYIA 321
Db 249 KKMLNINPKRLTAQVNLNHPWIKEDGADPTDPLDNNVLDRLKQFRAMNQFKKAALRIIA 308
QY 322 ERLSEERIGGLKELFKMTDTONSGTITFEELKAGLKRVSLEMESEIKSLMDAADINSG 381
Db 309 GCLSEERITGLKEMFKNIDKNSGTITLDELKHLGAKHPKLSDEMEKLEMAADADNG 368
QY 382 TIDYGEFTLAATHLMKMEREEILYVAAFSDFPKDGSGYITIDELQSACTEFGLCDT-PLDD 440
Db 369 LIDYDEFVTAIVHNMKLDREHLYTAFQYFDKNSGYITKEELEHALKEOGLYDADKID 428
QY 441 MIKEIDLDNDGKIDFSEFTAMMKRG 465
Db 429 IISDADSDNDGRIDYSEFVAMMRKG 453

RESULT 9
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US-08-459-448A-22
; Sequence 22, Application US/08459448A
; Patent No. 5859336
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5859336artis Corporation
; STREET: Patent & Trademark Dept., 520 White Plains
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591-9005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,448A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Gary M.
; REGISTRATION NUMBER: 40403
; REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8582
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 464 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..464
; OTHER INFORMATION: /note= "derived protein sequence of
; OTHER INFORMATION: pollen specific CDPK as disclosed in Figure 34."
US-08-459-448A-22
Query Match 55.4%; Score 1437.5; DB 2; Length 464;
Best Local Similarity 60.9%; Pred. No. 6.7e-112;
Matches 271; Conservative 70; Mismatches 103; Indels 1; Gaps 1;
22 LRDHYLLGKLGQGGFTTILCTIEKSTKSANYACKSIPKRLVCRDIEDYVWRELQIMHHL 81

Db 9 VRATYSMGKELRGQFGVTHLCTHRTSGEKLACKTIAKRLAARDVDDVRRREVQIMHHL 68
QY 82 SEHPNVRIRKGTVEDSVFVHIVMEVCEGGEFLFDRIYVSKGHFSREAVKLIKTLIGVVEAC 141
Db 69 SGQPNVGLRGAYEDKQSVHVLVMELCAGGELFDRIITARGQYITERGAELRLAIVQIVHTC 128
QY 142 HSLGVMRDLKPNFLFDSPKDAKDKATDFGLSVFKPGQYLYDVVGSPPYVAPEVLKK 201
Db 129 HSMGVMRDLKPNFLFDSKDEDAPLKATDFGLSVFKPGQYLYDVVGSPPYVAPEVLKR 188
QY 202 CYGPEIDVMSAGVILYLLSGVPPFWAETESGIFRILQGLKDFKSDPPTTSEAKDLI 261
Db 189 KYGPEADINSGVYMLYIFLAGVPPFWAENENGIFTAILRGQLDLSSEPPHISPGAKDLV 248
QY 262 YKMLERSPKKRISAHEALCPWIVDQAAAPDKPLDPAVLRLKOFKOFOMNKKIKMALRVIA 321
Db 249 KMLNINPKRLTAFQVLNHPWIKEDGADPTPLDNNVLDRLKQFRAMNQFKAAALRIIA 308
QY 322 ERLSEIEIGLKFELFKMIDTNSGTTTFEELKAGLRKRVGSELMESEIKSLMDAADINSG 381
Db 309 GCLSEBEITGLKEMFNKIDKNSGTTTLDLKHGLAKHGPKLSDSEWEXIMEAADADGNG 368
QY 382 TDYGEFLAATLHMKNKEREELVAAFSDFDKDGSYIITIDELOSACTEFLGCDT-PLDD 440
Db 369 LIDYDEFVTATVHMKNLDREEHLYTAFQYFDKDNSGYITKEELEHALKEGGLYDADKIKD 428
QY 441 MIKEIDLNDGKIDFSEFTAMRKG 465
Db 429 IISDADSDNDGRIDYSEFVAMRKG 453

RESULT 10
US-08-459-595A-22
; Sequence 22, Application US/08459595A
; Patent No. 6018104
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6018104artis Corporation
; STREET: Patent & Trademark Dept., 520 White Plains
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591-9005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,595A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 800

;; PRIOR APPLICATION DATA: US 07/951,715
;; APPLICATION NUMBER: US 07/951,715
;; FILING DATE: 25-SEP-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/772,027
;; FILING DATE: 04-OCT-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Pace, Gary M.
;; REGISTRATION NUMBER: 40403
;; REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV3
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (919)541-8582
;; TELEFAX: (919)541-8689
;; INFORMATION FOR SEQ ID NO: 22:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 464 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; HYPOTHETICAL: NO
;; FEATURE:
;; NAME/KEY: Protein
;; LOCATION: 1..464
;; OTHER INFORMATION: /note= "derived protein sequence of
;; OTHER INFORMATION: pollen specific CDPK as disclosed in Figure 34."
US-08-459-595A-22

Query Match 55.4%; Score 1437.5; DB 3; Length 464;
Best Local Similarity 60.9%; Pred. No. 6.7e-112;
Matches 271; Conservative 70; Mismatches 103; Indels 1; Gaps 1;
QY 22 LRDHVLLGKLGQGGTGYLCTEKSTANYACKSPKRLVCRDYEDVWREIQIMHHL 81
DB 9 VRATYSMGKELGQGGVTHCTHRTSGEKLAKTAKRLAAREDDVDRREVQIMHHL 68
QY 82 SEHPNVVRKGYEDSVFVHIVMEVCEGGELEFDRIYVSKGHFSEREAVKLITLGVVEAC 141
DB 69 SQGPNVVGRLGAYEDKQSVHLMELCAGGELEFDRIIARQYTERGAELLRAIVQIVHTC 128
QY 142 HSLGVNHRDLKPNFLFDSPKDKALIKATDFGLSVFYKPGVLYDVVGSPIYVAPVLA 201
DB 129 HSGVNHRIKDPENFLLSKEDAPLAKATDFGLSVFKEGELLRLDIVSAYIAPEVLKR 188
QY 202 CYGPEIDVWSAGVILYLLSGVPPFWAETESGIFRILQGLKDFKSDPWPPTISEAAKDLI 261
DB 189 KYGPEADVSGVWLYIFLAGVPPFWAENENGIFTALLRGQLDSSEPPHISPGAKDLV 248
QY 262 KYMLSPKPKRISAEHALCPHWIVDEQAAPDKPLDPAVLSRLKQFSQMKIKKMAURVTA 321
DB 249 KMLNINPKERTAFQVLEHNPWIKEDGDADPTPLDNVLDRLKQFRAMNQFKKALRIIA 308
QY 322 ERLSEIEIGLKFELKMIIDTNSGTITFEELKAGLKRVSSELMESIKSLMDAADIDNSG 381
DB 309 GCLSEIEITGLKEMFNIDKNSGTITLDELKGLAKHGFKLSDESEKLMERAADADNG 368
QY 382 TIDYGEFLAATHMKNMEREEILVAAFSDFDKGSGYITIDELQSACTEFLGCDT-PLDD 440
DB 369 LIDYDFVATVNMKNLDRHEHLYTAFQYEDKNSGYITKEEHLAKGEOGLYDADKID 428
QY 441 MIKEIDLNDGKIDFSEFFAMRKG 465
DB 429 IISDADSDNDGRIDYSEFVAMRKG 453

RESULT 11

US-08-459-504B-22
; Sequence 22, Application US/08459504B
; Patent No. 6075185
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.

;; APPLICANT: Kramer, Vance C.
;; APPLICANT: Warren, Gregory W.
;; APPLICANT: Evola, Stephen V.
;; APPLICANT: Crossland, Lyle D.
;; APPLICANT: Wright, Martha S.
;; APPLICANT: Merlin, Ellis J.
;; APPLICANT: Launis, Karen L.
;; APPLICANT: Rothstein, Steven J.
;; APPLICANT: Bowman, Cindy G.
;; APPLICANT: Dawson, John L.
;; APPLICANT: Dunder, Erik M.
;; APPLICANT: Pace, Gary M.
;; APPLICANT: Suttie, Janet L.
;; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
;; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
;; NUMBER OF SEQUENCES: 94
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: No. 6075185artis Corporation
;; STREET: 3054 Cordwallis Road
;; CITY: Research Triangle Park
;; STATE: NC
;; COUNTRY: USA
;; ZIP: 27709
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/459,504B
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/459,595
;; FILING DATE: 02-JUN-1995
;; APPLICATION NUMBER: US 07/951,715
;; FILING DATE: 25-SEP-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/772,027
;; FILING DATE: 04-OCT-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Meigs, J. Timothy
;; REGISTRATION NUMBER: 38,241
;; REFERENCE/DOCKET NUMBER: CGC1577/CIP/DIV
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (919)541-8587
;; TELEFAX: (919)541-8689
;; INFORMATION FOR SEQ ID NO: 22:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 464 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; HYPOTHETICAL: NO
;; FEATURE:
;; NAME/KEY: Protein
;; LOCATION: 1..464
;; OTHER INFORMATION: /note= "derived protein sequence of
;; OTHER INFORMATION: pollen specific CDPK as disclosed in Figure 34."
US-08-459-504B-22

Query Match 55.4%; Score 1437.5; DB 3; Length 464;
Best Local Similarity 60.9%; Pred. No. 6.7e-112;
Matches 271; Conservative 70; Mismatches 103; Indels 1; Gaps 1;

QY 22 LRDHVLLGKLGQGGTGYLCTEKSTANYACKSPKRLVCRDYEDVWREIQIMHHL 81
DB 9 VRATYSMGKELGQGGVTHCTHRTSGEKLAKTAKRLAAREDDVDRREVQIMHHL 68
QY 82 SEHPNVVRKGYEDSVFVHIVMEVCEGGELEFDRIYVSKGHFSEREAVKLITLGVVEAC 141
DB 69 SQGPNVVGRLGAYEDKQSVHLMELCAGGELEFDRIIARQYTERGAELLRAIVQIVHTC 128

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QY 142 HSLGVNHRDLKPNELFDSPKDDAKLKATDFGLSVFKPGQYLYDVVGSPPYVAPVLLK 201
Db 129 HSMGVNHRDLKPNELFDSPKDDAKLKATDFGLSVFKPGQYLYDVVGSPPYVAPVLLK 188
QY 202 CYGPEIDVWSAGVILXILLSGVPPFWAETSGIFRQILOGLKDFKSDPWPPTISEAAKDLI 261
Db 189 KYGPEADINSVGMVLIYFLAGVPPFWAENENGIFTALRGQLDLSSEPHISPGAKDLV 248
QY 262 YKMLERSPKKRISAHEALCHPWIVDQQAAPDKPLDPAVLRSKQFSOMNKKMALRVIA 321
Db 249 KKMNLNPKERLTAFOVNLHPWKEDGADPTPLDNVVLDRKQFRAMNQFKAALRIIA 308
QY 322 ERLSEERIGGLKELFKMIDNDNSGTITFEELKAGLKHVGSSEKSEKSLMDADINDSG 381
Db 309 GCLSEEBEITGLKEMFNIDKNSGTITLDELKHLGAKHGPKLSDSEMEKLEAADADNG 368
QY 382 TIDYGEFLAATLHMNMKMEREEILVAAFSDFDKDGSYITIDELQSACTEFGLCDT-PLDD 440
Db 369 LIDYDEFVATVHMNKLDRHEHLYTAFOYFDKNSGYITKEELEHALKEOGLYADAKIKD 428
QY 441 MIKEIDLNDGKIDFSEFTAMMRKG 465
Db 429 IISDADSDNDGRIDYSEFVAMMRKG 453
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RESULT 12

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US-08-459-444-22
; Sequence 0, Application US/08459444A
; Patent No. 6121014
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; Desai, Nalin M.
; Lewis, Kelly S.
; Kramer, Vance C.
; Warren, Gregory W.
; Evola, Stephen V.
; Crossland, Lyle D.
; Wright, Martha S.
; Merlin, Ellis J.
; Launis, Karen L.
; ZIP: 27709
; COUNTRY: USA
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,444A
; FILING DATE: 02-Jun-1995
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: S-18805/P1/CGC1577/CIP/DIV6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8587
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: /note= "derived protein sequence of
```

TITLE OF INVENTION: METHOD FOR PRODUCING A PLANT-OPTIMIZED

NUCLEIC ACID CODING SEQUENCE

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

```
ADDRESS: No. 6121014artis Agribusiness Biotechnology Research, Inc.
STREET: 3054 Cornwalls Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
```

COMPUTER READABLE FORM:

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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```
APPLICATION NUMBER: US/08/459,444A
```

```
FILING DATE: 02-Jun-1995
```

```
CLASSIFICATION: <Unknown>
```

```
PRIOR APPLICATION DATA:
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```
APPLICATION NUMBER: US 07/951,715
```

```
FILING DATE: 25-SEP-1992
```

```
APPLICATION NUMBER: US 07/772,027
```

```
FILING DATE: 04-OCT-1991
```

```
ATTORNEY/AGENT INFORMATION:
```

```
NAME: Meigs, J. Timothy
```

```
REGISTRATION NUMBER: 38,241
```

```
REFERENCE/DOCKET NUMBER: S-18805/P1/CGC1577/CIP/DIV6
```

```
TELECOMMUNICATION INFORMATION:
```

```
TELEPHONE: (919)541-8587
```

```
TELEFAX: (919)541-8689
```

```
INFORMATION FOR SEQ ID NO: /note= "derived protein sequence of
```

```
; pollen specific CDPK as disclosed in Figure 34."
; SEQUENCE CHARACTERISTICS:
; LENGTH: 464 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..464
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-08-459-444-22
```

```
Query Match 55.4%; Score 1437.5; DB 3; Length 464;
Best Local Similarity 60.9%; Pred. No. 6.7e-112;
Matches 271; Conservative 70; Mismatches 103; Indels 1; Gaps 1;
QY 22 LRHYLLGKLGKGGFGTTLCTEKSPTSANYACKSIPKRLKVCREDYEDVYREIQIMHHL 81
Db 9 VRATYSMGKELGRGFGVTHLCTHRTSGEKLACKTIARKLAAREDDVDRREVQIMHHL 68
QY 82 SEHPNVVRIKGTYESDVFVHVMVEVCGGELFDRIVSKGHFSREAVKLIKLTILGVVEAC 141
Db 69 SGQPNVVGLRGAYEDKQSVHVMELCAGGELFDRIIARGQYTERGAELRLAIVQIVHTC 128
QY 142 HSLGVNHRDLKPNELFDSPKDDAKLKATDFGLSVFKPGQYLYDVVGSPPYVAPVLLK 201
Db 129 HSMGVNHRDLKPNELFDSPKDDAKLKATDFGLSVFKPGQYLYDVVGSPPYVAPVLLK 188
QY 202 CYGPEIDVWSAGVILXILLSGVPPFWAETSGIFRQILOGLKDFKSDPWPPTISEAAKDLI 261
Db 189 KYGPEADINSVGMVLIYFLAGVPPFWAENENGIFTALRGQLDLSSEPHISPGAKDLV 248
QY 262 YKMLERSPKKRISAHEALCHPWIVDQQAAPDKPLDPAVLRSKQFSOMNKKMALRVIA 321
Db 249 KKMNLNPKERLTAFOVNLHPWKEDGADPTPLDNVVLDRKQFRAMNQFKAALRIIA 308
QY 322 ERLSEEBEITGLKEMFNIDKNSGTITFEELKAGLKHVGSSEKSEKSLMDADINDSG 381
Db 309 GCLSEEBEITGLKEMFNIDKNSGTITLDELKHLGAKHGPKLSDSEMEKLEAADADNG 368
QY 382 TIDYGEFLAATLHMNMKMEREEILVAAFSDFDKDGSYITIDELQSACTEFGLCDT-PLDD 440
Db 369 LIDYDEFVATVHMNKLDRHEHLYTAFOYFDKNSGYITKEELEHALKEOGLYADAKIKD 428
QY 441 MIKEIDLNDGKIDFSEFTAMMRKG 465
Db 429 IISDADSDNDGRIDYSEFVAMMRKG 453
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RESULT 13

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US-09-547-422-22
; Sequence 0, Application US/09547422
; Patent No. 6320100
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GENERAL INFORMATION:

```
APPLICANT: Koziel, Michael G.
Desai, Nalin M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Launis, Karen L.
```

```
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
```

```
INSECTICIDAL ACTIVITY IN MAIZE
```

```
NUMBER OF SEQUENCES: 94
```

```
CORRESPONDENCE ADDRESS:
```

```
ADDRESS: No. 6320100artis Agribusiness Biotechnology Research, Inc.
STREET: 3054 Cornwalls Road
CITY: Research Triangle Park
```

```
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/547,422
  FILING DATE: 11-Apr-2000
  CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 08/459,595
  FILING DATE: 02-JUN-1995
  APPLICATION NUMBER: US 07/951,715
  FILING DATE: 25-SEP-1992
  APPLICATION NUMBER: US 07/772,027
  FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
  NAME: Melgs, J. Timothy
  REGISTRATION NUMBER: 38,241
  REFERENCE/DOCKET NUMBER: S-18805H
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: (919)541-8587
    TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 7 note= "derived protein sequence of
pollen specific CDPK as disclosed in Figure 34."
SEQUENCE CHARACTERISTICS:
  LENGTH: 464 amino acids
  TYPE: amino acid
  STRANDEDNESS: single
  TOPOLOGY: linear
  MOLECULE TYPE: protein
  HYPOTHETICAL: NO
  FEATURE:
    NAME/KEY: Protein
    LOCATION: 1..464
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-547-422-22

Query Match      55.4%; Score 1437.5; DB 4; Length 464;
Best Local Similarity 60.9%; Pred. No. 6.7e-112;
Matches 271; Conservative 70; Mismatches 103; Indels 1; Gaps 1;

QY 22 LRDHLLGKLGQGGFTYLTCTEKSTSNYACKSTPKKLVKCYREDYDVWREIQIMHHL 81
Db 9 VRATYMGKELGKGQGVTHLCTHRTSGKTLAKRKLAAREDVDVREVQIMHHL 68

QY 82 SEHPNVVRKGYEDSVFVHIVMEVCEGGELEFDRIYVSKGHFSEREAVKLKTLGVVEAC 141
Db 69 SGQPNVVGLEAGYEDKQSVHVLWELCAGGELEFDRIIARQGYTERGAHELRLAIVQIVHFC 128

QY 142 HSLGVNHRDLKPNFLFDSPKDKALKATDFGLSVFKPGQYLYDVVGSPPYVAPEVLKK 201
Db 129 HSGVMNRDIPKPNELLKSKDEAPLKATDFGLSVFKEGELLRLDIVGSAYVIAPEVLKR 188

QY 202 CYGPETDVMSAGVILYLLSGVPPFAETESGIFRILQGLKDLDFKSDPPTTSEAAKDLI 261
Db 189 KTGPEADIVSGVGMDFIFLAGVPPFAENENGIFTAILRGQLDLSSEPPPHISPGAKDIV 248

QY 262 YKMLERSPKRISAEHALCHPWVLSQAAAPDKPLDPAVLRSRLKQFSOMNKKIKMLRVTA 321
Db 249 KKMNLINPKERLTAFOVLNHPWKEDGADPTPLDNNVLDRLKQFAMQFKKAALRIITA 308

QY 322 ERLSEIEGLKELFKMIDTNSGTTTFEELKAGLRVSGSELMSEIKSLMDAADIDNSG 381
Db 309 GCLSEIEITGLKEMFNIDKNSGTTTLDLKHGLAKHGPKLSDSEMEKLMEAADADNG 368

QY 382 TIDYGEFLAATLHNNKMEREEILVAFSDFDKGSGYIITIDELQSACTEFGLCDT-PLDD 440
Db 369 LIDYDEFTATVHNNKLDREEHLYTAFQYEDKDNSGYITKEELEHALKEQGLYDADKIND 428
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QY 441 MIKEIDLNDGKIDFSEFTAMMRKG 465
Db 429 IISDASDNDGRIDYSEFVAMMRKG 453
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RESULT 14

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US-07-951-715A-21
; Sequence 21, Application US/07951715A
; Patent No. 5625136
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalin M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/07/951,715A
  FILING DATE: 25-SEP-1992
  CLASSIFICATION: 800
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 07/772,027
    FILING DATE: 04-OCT-1991
  ATTORNEY/AGENT INFORMATION:
    NAME: Sprull, W. Murray
    REGISTRATION NUMBER: 32,943
    REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: (919)541-8615
    TELEFAX: (919)541-8689
  INFORMATION FOR SEQ ID NO: 21:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 408 amino acids
      TYPE: amino acid
      TOPOLOGY: linear
      MOLECULE TYPE: protein
US-07-951-715A-21

Query Match      49.3%; Score 1277.5; DB 1; Length 408;
Best Local Similarity 61.9%; Pred. No. 1.2e-98;
Matches 242; Conservative 59; Mismatches 89; Indels 1; Gaps 1;
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QY 76 QIMHHLSEHPNVVRKGYEDSVFVHIVMEVCEGGELEFDRIYVSKGHFSEREAVKLKTL 135
Db 1 QIMHLSGQPNVVGLEAGYEDKQSVHVLWELCAGGELEFDRIIARQGYTERGAHELRLAIV 60

QY 136 GVEVACHSGVMNRDIPKPNELLKSKDEAPLKATDFGLSVFKPGQYLYDVVGSPPYVA 195
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Db 61 QIVHTCHSMGVHRDIPKPNFLLSKDEDAPLKATDFGLSVFFKEGELLRDIVGSAYIIA 120
QY 196 PEVLKCYGPEIDVWSAGVILYILLSGVPPFWAETESGIFRQILQGLDFKSDPWPPTISE 255
Db 121 PEVLKRYGPEADTWSVGVMLYIFLAGVPPFWAENENGIFTAILRGQLDLSSEPWPHPISP 180
QY 256 AAKDLIYKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPVLSRLKQFSQMNKIKKM 315
Db 181 GAKDLVKMLNINPKERLTAFQVLNHWIKEDGDGADPTPLDNNVYLDRLKQFRANMOPKKA 240
QY 316 ALRVIAERLSEEEIGGLKELFKMIDTNSGTITFEELKAGLKRKVGSELMESEIKSLMDAA 375
Db 241 ALRIAGCLSEEEITGLKEMFNKIDKNSGTITLDELKHLGKLAGHPKLSSEMEKLMEEA 300
QY 376 DIDNSGTIDYGEFLAATLHNKMKEREELVAAFSDFPKDGSYITIDELQSACTFEGLCD 435
Db 301 DADNGLLIDYDEFVATVHNKILDRSHLYTAFQYFCKDNSGYITKEELEHALKEQGLYD 360
QY 436 T-PLDDMIKEIDLNDGKIDFSEFTAMMRKG 465
Db 361 ADKIKDIISDSDNDGRIDYSEFVAMMRKG 391
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RESULT 15

US-08-459-448A-21
Sequence 21, Application US/08459448A
Patent No. 5859336

GENERAL INFORMATION:

APPLICANT: Koziel, Michael G.
APPLICANT: Desai, Nalini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evoila, Stephen V.
APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Launis, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5859336artis Corporation
STREET: Patent & Trademark Dept., 520 White Plains
CITY: Tarrytown
STATE: New York
COUNTRY: USA
ZIP: 10591-9005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,448A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: 40403

REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919)541-8582
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 408 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-448A-21

Query Match 49.3%; Score 1277.5; DB 2; Length 408;

Best Local Similarity 61.9%; Pred. No. 1.2e-98;

Matches 242; Conservative 59; Mismatches 89; Indels 1; Gaps 1;

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QY 76 QIMHLSHPNNVRIKCTYEDSVHIVMEVCGEGELFDRIVSKGHSESEAVKLIKIL 135
Db 1 QIMHLSGQPNVGLRGAYEDKOSVHLVMELCAGGELFDRIIARGQYTERGAELLRAIV 60
QY 136 GVVYEAHSLGVMHRDLKPNFLFDPKDDAKLKATDFGLSVFYKPGQYLYDVVGSPPYVA 195
Db 61 QIVHTCHSMGVHRDIPKPNFLLSKDEDAPLKATDFGLSVFFKEGELLRDIVGSAYIIA 120
QY 196 PEVLKCYGPEIDVWSAGVILYILLSGVPPFWAETESGIFRQILQGLDFKSDPWPPTISE 255
Db 121 PEVLKRYGPEADTWSVGVMLYIFLAGVPPFWAENENGIFTAILRGQLDLSSEPWPHPISP 180
QY 256 AAKDLIYKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPVLSRLKQFSQMNKIKKM 315
Db 181 GAKDLVKMLNINPKERLTAFQVLNHWIKEDGDGADPTPLDNNVYLDRLKQFRANMOPKKA 240
QY 316 ALRVIAERLSEEEIGGLKELFKMIDTNSGTITFEELKAGLKRKVGSELMESEIKSLMDAA 375
Db 241 ALRIAGCLSEEEITGLKEMFNKIDKNSGTITLDELKHLGKLAGHPKLSSEMEKLMEEA 300
QY 376 DIDNSGTIDYGEFLAATLHNKMKEREELVAAFSDFPKDGSYITIDELQSACTFEGLCD 435
Db 301 DADNGLLIDYDEFVATVHNKILDRSHLYTAFQYFCKDNSGYITKEELEHALKEQGLYD 360
QY 436 T-PLDDMIKEIDLNDGKIDFSEFTAMMRKG 465
Db 361 ADKIKDIISDSDNDGRIDYSEFVAMMRKG 391
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Search completed: March 26, 2003, 13:13:54

Job time : 28 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 26, 2003, 13:12:27 ; Search time 118 Seconds
(without alignments)

246.341 Million cell updates/sec

Title: US-09-848-806-1

Perfect score: 2593

Sequence: 1 METKKNPRRPSNTVLPYQTP.....KNLNFNIAAFVGDEKSD 495

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 237916 seqs, 58723674 residues

Total number of hits satisfying chosen parameters: 237916

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA.*

1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1927	74.3	463	9	US-09-988-462-25
2	1672.5	64.5	639	10	US-09-854-731-17
3	1509.5	58.2	549	10	US-09-828-313-39
4	1437.5	55.4	464	9	US-09-988-462-22
5	1277.5	49.3	408	9	US-09-988-462-21
6	849	32.7	597	10	US-09-828-313-38
7	829	32.0	623	10	US-09-854-731-4
8	826	31.9	625	10	US-09-854-731-18
9	800	30.9	576	10	US-09-854-731-19
10	587.5	22.7	317	9	US-09-935-464-36
11	587.5	22.7	370	9	US-10-142-356-7
12	587.5	22.7	370	10	US-09-817-181-4
13	554	21.4	357	10	US-10-024-036B-2
14	543.5	21.0	556	12	US-10-096-960-4
15	543	20.9	460	9	US-09-935-464-3
16	543	20.9	476	9	US-09-935-464-5
17	539	20.8	565	12	US-10-096-960-2
18	538.5	20.8	326	10	US-09-817-181-2
19	533.5	20.6	387	10	US-09-771-161A-188

20 530 20.4 295 9 US-09-988-462-23 Sequence 23, Appl
21 510.5 19.7 648 9 US-10-024-036B-5 Sequence 5, Appl
22 510.5 19.7 817 10 US-09-992-481-4 Sequence 4, Appl
23 501 19.3 765 9 US-10-217-357-4 Sequence 4, Appl
24 501 19.3 765 10 US-09-975-326-4 Sequence 4, Appl
25 501 19.3 766 9 US-09-934-406-2 Sequence 2, Appl
26 501 19.3 766 9 US-10-217-357-2 Sequence 2, Appl
27 501 19.3 766 10 US-09-975-326-2 Sequence 2, Appl
28 496 19.1 385 9 US-10-116-332-2 Sequence 2, Appl
29 489.5 18.9 454 9 US-09-771-161A-238 Sequence 238, App
30 473.5 18.3 545 9 US-10-142-356-6 Sequence 6, Appl
31 473 18.2 543 10 US-09-740-627-1 Sequence 1, Appl
32 468.5 18.1 280 10 US-09-835-788A-16 Sequence 16, Appl
33 461.5 17.8 406 10 US-09-771-161A-210 Sequence 210, App
34 460 17.7 261 9 US-09-925-299-983 Sequence 983, App
35 460 17.7 261 10 US-09-925-299-983 Sequence 16, Appl
36 459.5 17.7 821 9 US-10-081-119-16 Sequence 16, Appl
37 457.5 17.6 740 10 US-09-771-161A-265 Sequence 265, App
38 457.5 17.6 740 10 US-09-771-161A-266 Sequence 266, App
39 453 17.5 522 10 US-09-740-627-11 Sequence 11, Appl
40 447.5 17.3 501 10 US-09-797-039-2 Sequence 2, Appl
41 447.5 17.3 501 12 US-10-153-921-2 Sequence 2, Appl
42 446 17.2 1518 10 US-09-801-368-152 Sequence 152, App
43 445.5 17.2 1203 10 US-09-799-875-5 Sequence 5, Appl
44 443 17.1 514 10 US-09-922-138-5 Sequence 5, Appl
45 443 17.1 514 10 US-09-841-683-2 Sequence 2, Appl

ALIGNMENTS

RESULT 1

US-09-988-462-25
Sequence 25, Application US/09988462
Publication No. US20030046726A1

GENERAL INFORMATION:

APPLICANT: Koziel, Michael G.
Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Lauis, Karen L.

TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
INSECTICIDAL ACTIVITY IN MAIZE

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESSEE: Syngenta Biotechnology, Inc.
STREET: 5054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC

COUNTRY: USA

ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/988,462

FILING DATE: 20-NO. US20030046726A1-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/547,422

FILING DATE: 11-APR-2000

APPLICATION NUMBER: US 08/459,504

FILING DATE: 02-JUN-1995

APPLICATION NUMBER: US 07/951,715

FILING DATE: 25-SEP-1992

APPLICATION NUMBER: US 07/772,027

FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-188051
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 463 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: Protein
LOCATION: 1..463
OTHER INFORMATION: /note= "protein sequence for
soybean CDPK as shown in Figure 34."
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-988-462-25

Query Match 74.3%; Score 1927; DB 9; Length 463;
Best Local Similarity 78.7%; Pred. No. 2.9e-128;
Matches 365; Conservative 49; Mismatches 48; Indels 2; Gaps 2;

QY 14 VLPHYQTPRLRDHYLLKGLGQGFQFTYLCSTKSTSAKYACKSIPKRLKLVCHREDYEDVWR 73
Db 1 VLPHQTNLREYEVGRKLGQGFQFTCTRRASGGKFAKSPKRLKLVCHREDYEDVWR 60
QY 74 EIQIMHLSHPNVRIKGTIEDSVFVHVMVECGEGELFDRIYKSGHFSEREAVKLIKT 133
Db 61 EIQIMHLSHPNVRIKGTIEDSVFVHVMVECGEGELFDRIYKSGHFSEREAVKLIKT 120
QY 134 ILGVVEACHSLGVMHRLDKPENLFDSPKDDAKLKAIDFGLSVFYKPGQYLDVVGSPYY 193
Db 121 IYEVVEACHSLGVMHRLDKPENLFDIDEDAKLKAIDFGLSVFYKPGSFCDVVGSPYY 180
QY 194 VAPEVLKCYGPEIDVWSAGVYLYLLSGVPPFWAETESGIFRQILQGLDFKSDPWPTI 253
Db 181 VAPEVLKLYGPEIDVWSAGVYLYLLSGVPPFWAETESGIFRQILQGLDFHSEFPWPSI 240
QY 254 SEAAKDLIYKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAYISRLKQFSQMNKIK 313
Db 241 SDSAKDLIRKMLDONPKRLTAHEVLRHPWIVDDNIAPDKPLDSAVLSRLKQFSQMNKIK 300
QY 314 KVALRVIAERLSEETIGGLKELFKMTIDTNSGTITFEELKAGLKRVSGLMESEIKSLMD 373
Db 301 KVALRVIAERLSEETIGGLKELFKMTIDTNSGTITFEELKAGLKRVSGLMESEIKSLMD 360
QY 374 AADINSGVIDYGEFLAATPLHNKMEREBILVAAFSDPKDGSYITITDELQSACTEFLG 433
Db 361 AADIDKSGTIDYGEFLAATPLHNKMEREBILVAAFSDPKDGSYITITDELQSACTEFLG 420
QY 434 CDTPLDDMIKEIDLDNDGKIDFSEPTAMRKGD-GVGRSRTMMK 476
Db 421 DDHIDDMIKEDQNDGQIDYGEFAAMRKGGTGIR-RTMRK 463

RESULT 2
US-09-854-731-17
; Sequence 17, Application US/09854731
; Patent No. US20020120949A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Lee, Jian Ming
; TITLE OF INVENTION: Plant Protein Kinases
; FILE REFERENCE: BB-1171
; CURRENT APPLICATION NUMBER: US/09/854,731
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/092,438

; PRIOR FILING DATE: July 10, 1998
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 17
; LENGTH: 639
; TYPE: PRT
; ORGANISM: Zea mays
US-09-854-731-17

Query Match 64.5%; Score 1672.5; DB 10; Length 639;
Best Local Similarity 66.2%; Pred. No. 3.6e-110;
Matches 318; Conservative 66; Mismatches 83; Indels 13; Gaps 3;
QY 5 PNPR-RPS-----NTVLPYQTPRLRDHYLLKGLGQGFQFTYLCSTKSTSAKY 52
Db 120 PPSRPRPQVKRYSSACLLLSGLSVLRKTKENLKDYSLGRRLGQGFQFTYLCSTKSTSAKY 179
QY 53 ACKSIPKRLKLVCHREDYEDVWRVREIQIMHLSHPNVRIKGTIEDSVFVHVMVECGEGEL 112
Db 180 ACKSILKRLKLGSDDDVEDVRREIQIMHLSHPNVRIKGTIEDSVFVHVMVECGEGEL 239
QY 113 FDRIVYKSGHFSEREAVKLIKTILGVVEACHSLGVMHRLDKPENLFDSPKDDAKLKAIDF 172
Db 240 FDRIVYKSGHFSEREAVKLIKTILGVVEACHSLGVMHRLDKPENLFDSPKDDAKLKAIDF 299
QY 173 GLSVFYKPGQYLYLLSGVPPFWAETESGIFRQILQGLDFKSDPWPTI 232
Db 300 GLSVFYKPGQYLYLLSGVPPFWAETESGIFRQILQGLDFKSDPWPTI 359
QY 233 GTFRQILQGLDFKSDPWPTI 292
Db 360 GTFEEVLRGLDFSEPEPWSISDGAARDLVRMLVRDPKRLTAHEVLRHPWIVDDNIAPDKPLDSAVLSRLKQFSQMNKIK 419
QY 293 KPLDPAVLISRLKQFSQMNKIKKVALRVIAERLSEETIGGLKELFKMTIDTNSGTITFEEL 352
Db 420 RPLDPAVLISRLKQFSQMNKIKKVALRVIAERLSEETIGGLKELFKMTIDTNSGTITFEEL 479
QY 353 KAGLRVSELSMESEIKSLMDAADDINSGTIDYGEFLAATPLHNKMEREBILVAAFSDPD 412
Db 480 KVLGKLVGANLQSEBIYALMAQADVNDNGTIDYGEFLAATPLHNKMEREBILVAAFSDPD 539
QY 413 KDGSGYITITDELQSACTEFLGCDTFLDDMIKEIDLDNDGKIDFSEPTAMRKGDGVGRSR 472
Db 540 KDGSGYITITDELQSACTEFLGCDTFLDDMIKEIDLDNDGKIDFSEPTAMRKGDGVGRSR 598

RESULT 3
US-09-828-313-39
; Sequence 39, Application US/09828313
; Patent No. US20020059662A1
; GENERAL INFORMATION:
; APPLICANT: COSTA e SILVA, OSWALDO DA
; APPLICANT: BOHNERT, HANS J.
; APPLICANT: THIELEN, NOCHA VAN
; APPLICANT: CHEN, ROUYING
; APPLICANT: SARRIA-MILLAN, RODRIGO
; TITLE OF INVENTION: PROTEIN KINASE STRESS-RELATED PROTEINS AND METHODS OF
; TITLE OF INVENTION: USE IN PLANTS
; FILE REFERENCE: 16313-0032
; CURRENT APPLICATION NUMBER: US/09/828,313
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/196,001
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 549
; TYPE: PRT
; ORGANISM: Physcomitrella patens
US-09-828-313-39

Query Match 58.2%; Score 1509.5; DB 10; Length 549;
Best Local Similarity 60.8%; Pred. No. 9.1e-99;

Db 538 KEGNRVYPPDEL---AKEMGLAPNPAQVFLDWIRQ-----SDGRLSGTGFTKLLH----- 585
QY 469 GRSTMMKNL 478
Db 586 GISSRAIKNL 595

RESULT 7
US-09-854-731-4
; Sequence 4, Application US/09854731
; Patent No. US20020120949A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; TITLE OF INVENTION: Plant Protein Kinases
; FILE REFERENCE: BB-1171
; CURRENT APPLICATION NUMBER: US/09/854,731
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/092,438
; PRIOR FILING DATE: July 10, 1998
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 4
; LENGTH: 623
; TYPE: PRT
; ORGANISM: Oryza sativa
US-09-854-731-4

Query Match 32.0%; Score 829; DB 10; Length 623;
Best Local Similarity 40.6%; Pred. No. 9e-51;
Matches 183; Conservative 87; Mismatches 155; Indels 26; Gaps 11;
QY 26 YLGGKILGOGQFGTTLCTEKSANY-----ACKSIPKKLVCRDIEDYDWRREIQIMHH 80
Db 172 YELGKEVGRGHFGHT--CSAVVKKGKGTQVAVKIIAKAKMTTATSIEDVRREVKILRA 229
QY 81 LSEHNVVRIKGTIEDSVFVHIYMEVCEGGELFDRIYSK--GHFSEAEVKLIKTLGVVE 139
Db 230 LSGHNNLVKFYDACEGDLNVIYIMELCEGELLDRILARGRYTEDEAKAIVQILSVVA 289
QY 140 ACHSLGVHRLDKPENFLDPSKDDAKLKAATDFGLSVFYKPGQYLYDVVGSPPYVAPEVL 199
Db 290 FCHLQGVVHRLDKPENFLDPSKDDAKLKAATDFGLSVFYKPGQYLYDVVGSPPYVAPEVL 349
QY 200 KKGYPEDVWSAGVLYLILSGVPPFWAETESGIFRQILQKLDKDFKSDPWTISEAAKD 259
Db 350 HRSYSMEADLWSIGVITYILLGSRPFWARTESGIFRSVLRADPNFDDSPWPTVSAEAKD 409
QY 260 LIYKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAVLRLKOFSONMKIKKMLRV 319
Db 410 FVKRFLNKDYKRKMTAVQALTHPWLDEQR--QIPDLILIFRLIKQYLRATPKRLALKA 467
QY 320 IAERLSEELIGLKEFLKMDIDTNSGTITFEELKAGLRKRVSELM--ESEIKSLMDAADID 378
Db 468 LSKALREDELLYLQFKLLE--PRDGFVSLDNFRTALTRYLTDAMKRSRVLEFQHALEPL 526
QY 379 NSGTIDYGEFLAATL---HMNMKMER--EELIVAAFSDFDKDGSYITIDELQSACTEFGLC 434
Db 527 AYRMDPEFECAAAISPYOLEALERWEEETAGTAFQHFQEGNVRVISVEEL---AQELNLA 583

QY 435 DTP---LDDMIKEIDLNDGKIDFSFTAMM 462
Db 584 PTHYSIVQDWIRK----SDGKLNFLGFTKFL 610
RESULT 8
US-09-854-731-18
; Sequence 18, Application US/09854731
; Patent No. US20020120949A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Lee, Jian Ming

; TITLE OF INVENTION: Plant Protein Kinases
; FILE REFERENCE: BB-1171
; CURRENT APPLICATION NUMBER: US/09/854,731
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/092,438
; PRIOR FILING DATE: July 10, 1998
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 18
; LENGTH: 625
; TYPE: PRT
; ORGANISM: Zea mays
US-09-854-731-18

Query Match 31.9%; Score 826; DB 10; Length 625;
Best Local Similarity 40.8%; Pred. No. 1.5e-50;
Matches 183; Conservative 85; Mismatches 159; Indels 22; Gaps 10;
QY 26 YLGGKILGOGQFGTTLCTEKS---TSANYACKSIPKRLVCRDIEDYDWRREIQIMHLS 82
Db 174 YDLGKEVGRGHFGHTCSAVVKKGKGTQVAVKIIKAKMTTATSIEDVRREVKILKALS 233
QY 83 EHPNVVRIKGTIEDSVFVHIYMEVCEGGELFDRIYSK--GHFSEAEVKLIKTLGVVEAC 141
Db 234 GHDLNLYREFYDACEGDLNVIYIMELCEGELLDRILARGRYTEDEAKAIVQILSVVAF 293
QY 142 HSLGVHRLDKPENFLDPSKDDAKLKAATDFGLSVFYKPGQYLYDVVGSPPYVAPEVLK 201
Db 294 HLGQVHRLDKPENFLDPSKDDAKLKAATDFGLSVFYKPGQYLYDVVGSPPYVAPEVLK 353
QY 202 CYGPEIDVWSAGVLYLILSGVPPFWAETESGIFRQILQKLDKDFKSDPWTISEAAKDL 261
Db 354 SYSMEADLWSIGVITYILLGSRPFWARTESGIFRSVLRADPNFDDSPWPTVSAEAKDF 413
QY 262 YKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAVLRLKOFSONMKIKKMLRVIA 321
Db 414 KRLNKDYKRKMTAVQALTHPWLDEQR--QIPDLILIFRLVQYLRATPKRLALKALS 471
QY 322 ERUSEEELIGLKEFLKMDIDTNSGTITFEELKAGLRKRVSELM--ESEIKSLMDAADIDNS 380
Db 472 KALSEDELLYLQFKLLE--PRDGFVSLDNFRTALTRYLTDAMKRSRVLEFQHALEPLAY 530
QY 381 GTIDYGEFLAATL---HMNMKMER--EELIVAAFSDFDKDGSYITIDELQSACTEFGLCDT 436
Db 531 RMDPEFECAAAISPYOLEALERWEEETAGTAFQHFQEGNVRVISVEEL---AQELNLA 587
QY 437 P---LDDMIKEIDLNDGKIDFSFTAMM 462
Db 588 HYSIVQDWIRK----SDGKLNFLGFTKFL 612

RESULT 9
US-09-854-731-19
; Sequence 19, Application US/09854731
; Patent No. US20020120949A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Lee, Jian Ming
; TITLE OF INVENTION: Plant Protein Kinases
; FILE REFERENCE: BB-1171
; CURRENT APPLICATION NUMBER: US/09/854,731
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/092,438
; PRIOR FILING DATE: July 10, 1998
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 19
; LENGTH: 576
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-854-731-19

Query Match 30.9%; Score 800; DB 10; Length 576;


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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 460
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-935-464-3
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Query Match      20.9%; Score 543; DB 9; Length 460;
Best Local Similarity 39.6%; Pred.No. 8.6e-31;
Matches 116; Conservative 62; Mismatches 107; Indels 8; Gaps 6;

QY 18 QTPRLRDHYLLGKLLGQGGFTYILCTEKSTANTYACKSIPKRLVCRDIEDVWREIQI 77
Db 15 QTTNIRKTFIEMVLGSGAFSEVFLVKQLTGKLFALCKIKKSPAFROSSLEN---ETAV 71
QY 78 MHLSEHPNVVRKITYEDSVFVHVMEVCEGGELEFDRIVSKGHFSEERAVKLITILGV 137
Db 72 LKKI-KHENIVTLEDIYESTTHYILVMQLVSGGELFDRILRGVYTEKDALVIQQVLSA 130
QY 138 VEAHSLGVNHRDLKPNFLDPSKDDAKLKATDFGLSVFYKPGQYLYDVVGSPYYVAPE 197
Db 131 VKYLGHNGIVHRDLKPNLLYLTPENSKIMTDFGLSKMEONG-IMSTACGTGYVAPE 189
QY 198 VL-KCYGPEIDVWSAGVILYILLSGVPPFWAETESGIFRQILQKLDKFDKSDPWTISEA 256
Db 190 VLAQKPYSKAVDCWSIGVITYILLCGYPPFYETESKLFKEIKGYEYESFPFWDISES 249
QY 257 AKDLIYKMLERSPKKRISAEALCHPWIVDEQAAPDKPLDPAV-LSRLKQFSQ 308
Db 250 AKDFICHLEKDPNERYTCEKALSHPWI-DGNTALHRDIYPSVSLQIQNFAK 301
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Search completed: March 26, 2003, 13:22:07
Job time : 122 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 26, 2003, 12:16:51 ; Search time 40 Seconds
(without alignments)
1189.663 Million cell updates/sec

Title: US-09-848-806-1

Perfect score: 2593

Sequence: 1 METKPNRRPSNTVLPYQTFP.....KNLNENIADAFGVDGKSD 495

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_73: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2593	100.0	495	1 S46284	calcium-dependent
2	2458	94.8	501	2 G85097	hypothetical prote
3	2030	78.3	490	2 T08873	calcium-dependent
4	1944	75.0	508	1 A43713	calcium-dependent
5	1847.5	71.2	490	1 S71776	calcium-dependent
6	1752	67.6	492	1 T03271	calcium-dependent
7	1751	67.5	487	1 S71770	calcium-dependent
8	1745	67.3	554	1 T03263	calcium-dependent
9	1742	67.2	556	2 T06136	calcium-dependent
10	1731	66.8	544	2 D84550	calcium-dependent
11	1724	66.5	610	1 A49082	probable calmoduli
12	1709.5	65.9	573	2 T09940	calcium-dependent
13	1700.5	65.6	484	2 T05650	calcium-dependent
14	1672.5	64.5	639	1 T02784	calcium-dependent
15	1640.5	63.3	583	2 H84810	calcium-dependent
16	1630	62.9	451	2 S56717	probable calcium-d
17	1586	61.2	542	1 S56651	calcium-dependent
18	1484.5	57.3	540	1 T01989	calcium-dependent
19	1482	57.2	531	2 D85059	calcium-dependent
20	1480	57.1	531	1 S56652	probable calcium d
21	1480	57.1	531	1 T02993	calcium-dependent
22	1463.5	56.4	521	2 G96543	calcium-dependent
23	1462	56.4	529	1 S71774	calcium-dependent
24	1460.5	56.3	513	1 T02259	calcium-dependent
25	1460	56.3	534	1 JC1515	calcium-dependent
26	1458.5	56.2	538	2 T08874	calcium-dependent
27	1449	55.9	554	2 T05476	calcium-dependent
28	1437.5	55.4	465	1 T03024	calcium-dependent
29	1432.5	55.2	532	2 T14335	protein kinase, ca

30	1431	55.2	514	2 T10938	calcium-dependent
31	1381	53.3	545	2 H86322	calcium-dependent
32	1367.5	52.7	493	1 S46283	calcium-dependent
33	1363	52.6	541	2 F96776	hypothetical prote
34	1361	52.5	553	1 T02139	calcium-dependent
35	1356.5	52.3	520	2 F85059	calcium-dependent
36	1325.5	51.1	560	2 T46189	probable calcium d
37	1324.5	51.1	425	2 S17759	calcium-dependent
38	1313.5	50.7	533	1 S71778	protein kinase, ca
39	1287.5	49.7	520	2 C84774	calcium-dependent
40	1280.5	49.4	530	2 A84847	probable calcium-d
41	1238.5	47.8	582	2 E84721	probable Ca2+ depe
42	1229.5	47.4	575	2 C85059	probable calcium-d
43	1225.5	47.3	503	2 T51156	probable calcium d
44	1176.5	45.4	591	2 S54788	calcium-dependent
45	1056.5	40.7	571	2 T00835	calcium-stimulated
					calcium-dependent

ALIGNMENTS

RESULT 1

S46284

calcium-dependent protein kinase (EC 2.7.1.-) 2 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 16-Jun-2000

C:Accession: S46284

R:Urao, T.; Katagiri, T.; Mizoguchi, T.; Yamaguchi-Shinozaki, K.; Hayashida, N.; Shi

Mol. Gen. Genet. 244, 331-340, 1994

A:Title: Two genes that encode Ca(2+)-dependent protein kinases are induced by droug

A:Reference number: S46283; MUID:94359455; PMID:8078458

A:Accession: S46284

A:Molecule type: mRNA

A:Residues: 1-495 <URA>

A:Cross-references: EMBL:D21806; NID:gl235717; PIDN:BAA04830.1; PID:g604881

C:Genetics:

A:Gene: Cbpx2

C:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein

C:Keywords: ATP; calcium binding; EF hand; phosphotransferase; serine/threonine-spec

F:24-284/Domain: protein kinase homology <KIN>

F:32-40/Region: protein kinase ATP-binding motif

F:327-359/Domain: calmodulin repeat homology <EFI>

F:363-395/Domain: calmodulin repeat homology <EF2>

F:399-431/Domain: calmodulin repeat homology <EF3>

F:433-465/Domain: calmodulin repeat homology <ER4>

F:55/Active site: Lys #status Predicted

Query Match

Best Local Similarity 100.0%; Score 2593; DB 1; Length 495;

Matches 495; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 METKPNRRPSNTVLPYQTFPRLRDHYLLGKLGQGFQGTTLCTEKSTSANVACKSIPKR 60

Db 1 METKPNRRPSNTVLPYQTFPRLRDHYLLGKLGQGFQGTTLCTEKSTSANVACKSIPKR 60

Qy 61 KLVCREDYEDVWRETIQIMHHLSEHPNVVRIKGTVEDSVFVHVMVECGGELFDRIVSKG 120

Db 61 KLVCREDYEDVWRETIQIMHHLSEHPNVVRIKGTVEDSVFVHVMVECGGELFDRIVSKG 120

Qy 121 HFSREAVKLIKTILGVVEACHSLGVHMDLKPENLFDSPKDDAKLKATDFGLSVFYKP 180

Db 121 HFSREAVKLIKTILGVVEACHSLGVHMDLKPENLFDSPKDDAKLKATDFGLSVFYKP 180

Qy 181 GQYLDVVGSPYYVAPEVLKKCYGPEIDVWSAGVILYLLSSVPPFVAETESGIFRQLQ 240

Db 181 GQYLDVVGSPYYVAPEVLKKCYGPEIDVWSAGVILYLLSSVPPFVAETESGIFRQLQ 240

Qy 241 GKLFKSDPWPPTISEAAKDLIYKMLERSPKKRISAHEALCHPWIVDQAPDKPLDPAVL 300

Db 241 GKLFKSDPWPPTISEAAKDLIYKMLERSPKKRISAHEALCHPWIVDQAPDKPLDPAVL 300

Qy 301 SRLQFSCMNKKMKALVIAERISEEIGGLKELFKMIDFNSGTITFEELKAGLRVG 360

Db 301 SRLQFSCMNKKMKALVIAERISEEIGGLKELFKMIDFNSGTITFEELKAGLRVG 360

Db 301 SRLKQFSQMNKIKKALVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLKRVG 360
QY 361 SELMESEIKSLMDAADIDNSGTIDYGEFLAATLHMKNKEREILVAAFSDFDKGSGYIT 420
Db 361 SELMESEIKSLMDAADIDNSGTIDYGEFLAATLHMKNKEREILVAAFSDFDKGSGYIT 420
QY 421 IDELQSACTEFLGCDTFLDDMKEDLDNDGKIDFSEFTAMMRKGDGVRSTMMKNLNF 480
Db 421 IDELQSACTEFLGCDTFLDDMKEDLDNDGKIDFSEFTAMMRKGDGVRSTMMKNLNF 480
QY 481 NIADAFGVDGKSD 495
Db 481 NIADAFGVDGKSD 495
RESULT 2
G85097
hypothetical protein At4g09570 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 23-Mar-2001
C:Accession: G85097
R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
Nature 402, 769-777, 1999
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: A85001; MUID:20083488; PMID:10617198
A:Accession: G85097
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-501 <STO>
A:Cross-references: GB:NC_001268; NID:g7267652; PIDN:CAB78080.1; GSPDB:GN00140
C:Genetics:
A:Gene: At4g09570
A:Map position: 4
C:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kin
C:Keywords: EF hand

Query Match 94.8%; Score 2458; DB 2; Length 501;
Best Local Similarity 94.8%; Pred. No. 1.6e-84;
Matches 470; Conservative 9; Mismatches 13; Indels 4; Gaps 1;
QY 4 KPNRRPSNTVLPYQTPRLRDHYLLGKLGQGGQGTYYLCTEKTSTANYACKSTIPKRLV 63
Db 3 KPNRRPSNVLPYQTPRLRDHYLLGKLGQGGQGTYYLCTEKTSTANYACKSTIPKRLV 62
QY 64 CREDYEDVWREIQIMHLSHPNVVRIGKGYEDSVFVHVMVECGEGELFDRIYVSKGHES 123
Db 63 CREDYEDVWREIQIMHLSHPNVVRIGKGYEDSVFVHVMVECGEGELFDRIYVSKGCF 122
QY 124 EREAVLIKILGVVEACHSLGVNHRDLKPNFLDPSKDDAKLKATDFGLSVFYKPGQY 183
Db 123 EREAAKLIKILGVVEACHSLGVNHRDLKPNFLDPSKDDAKLKATDFGLSVFYKPGQY 182
QY 184 LYDVVSGPYVAVPLVKKCYGPEIDVWSAGVILYLLSGVPPFWAETESGIFRQILQGLK 243
Db 183 LYDVVSGPYVAVPLVKKCYGPEIDVWSAGVILYLLSGVPPFWAETESGIFRQILQGLK 242
QY 244 DFKSDPPTTISEAKOLIIYKMLRSPKRIISAHEALCHPWIVDQAAAPDKPLDPVAVLSRL 303
Db 243 DFKSDPPTTISEAKOLIIYKMLRSPKRIISAHEALCHPWIVDQAAAPDKPLDPVAVLSRL 302
QY 304 KQFSQMNKIKKALVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLKRVGSEL 363
Db 303 KQFSQMNKIKKALVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLKRVGSEL 362
QY 364 MESEIKSLMDAADIDNSGTIDYGEFLAATLHMKNKEREILVAAFSDFDKGSGYITIDE 423
Db 363 MESEIKSLMDAADIDNSGTIDYGEFLAATLHMKNKEREILVAAFSDFDKGSGYITIDE 422
QY 424 LQSACTEFLGCDTFLDDMKEDLDNDGKIDFSEFTAMMRKGDGVRSTMMKNLNF 483
Db 423 LQSACTEFLGCDTFLDDMKEDLDNDGKIDFSEFTAMMRKGDGVRSTMMKNLNF 482
QY 484 DAFGVDG----EKSDD 495

Db 483 EAFGVEDTSTAKSDD 498
RESULT 3
T08873
calcium-dependent protein kinase (EC 2.7.1.1-) beta - soybean
C:Species: Glycine max (soybean)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jan-2000
C:Accession: T08873
R:Lee, J.Y.; Yoo, B.C.; Harmon, A.C.
submitted to the EMBL Data Library, September 1996
A:Reference number: Z16505
A:Accession: T08873
A:Molecule type: mRNA
A:Residues: 1-490 <LEE>
A:Cross-references: EMBL:U69173; NID:g2501763; PID:g2501764
C:Genetics:
A:Gene: CDPK beta
C:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein
C:Keywords: ATP; calcium binding; EF hand; phosphotransferase; serine/threonine-speci
F:22-282/Domain: protein kinase homology <KIN>
F:30-38/Region: protein kinase ATP-binding motif
F:324-356/Domain: calmodulin repeat homology <EFH>
F:53/Active site: Lys #status predicted

Query Match 78.3%; Score 2030; DB 2; Length 490;
Best Local Similarity 81.1%; Pred. No. 1e-68;
Matches 386; Conservative 43; Mismatches 45; Indels 2; Gaps 2;
QY 14 VLPYQTPRLRDHYLLGKLGQGGQGTYYLCTEKTSTANYACKSTIPKRLVCREDEYDVR 73
Db 12 VLPYQTPARLDHYLLGKLGQGGQGTYYLCTHKTGYTKLYACKSTIPKRLVCREDEYDVR 71
QY 74 EIQLMHLSHPNVVRIGKGYEDSVFVHVMVECGEGELFDRIYVSKGHESEREAVLIK 133
Db 72 EIQLMHLSHPNVVRIGKGYEDSVFVHVMVECGEGELFDRIYVSKGHESEREAVLIK 131
QY 134 ILGVVEACHSLGVNHRDLKPNFLDPSKDDAKLKATDFGLSVFYKPGQYIDYVVGSPY 193
Db 132 IVGVVEACHSLGVNHRDLKPNFLDPSKDDAKLKATDFGLSVILOARQAFHDVVGSPY 191
QY 194 VAPVLKCYGPEIDVWSAGVILYLLSGVPPFWAETESGIFRQILQGLKDFSDPPTI 253
Db 192 VAPVLKCYGPEIDVWSAGVILYLLSGVPPFWAETESGIFRQILQGLKDFSDPPTI 251
QY 254 SEAAKDLIYKMLRSPKRIISAHEALCHPWIVDQAAAPDKPLDPVAVLSRLKQFSQMNKIK 313
Db 252 SENAKELVKQMLDRDPKRIISAHEALCHPWIVDQAAAPDKPLDPVAVLSRLKQFSQMNKIK 310
QY 314 KMALRVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLKRVGSELMESEIKSLMD 373
Db 311 KMALRVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLKRVGSELMESEIKSLMD 370
QY 374 AADIDNSGTIDYGEFLAATLHMKNKEREILVAAFSDFDKGSGYITIDELOQACTEFL 433
Db 371 AADIDNSGTIDYGEFLAATLHMKNKEREILVAAFSDFDKGSGYITIDELOQACTEFL 430
QY 434 CDTPLDDMKEDLDNDGKIDFSEFTAMMRKGDGVRSTMMKNLNFNIADAFV 488
Db 431 GDVHLDMEIKEDLDNDGKIDFSEFTAMMRKGDGVRSTMMKNLNFNIADAFV 486
RESULT 4
A43713
calcium-dependent protein kinase (EC 2.7.1.1-) - soybean
C:Species: Glycine max (soybean)
C:Date: 03-Mar-1993 #sequence_revision 14-Jul-1994 #text_change 11-Jun-1999
C:Accession: A43713
R:Harper, J.F.; Sussman, M.R.; Schaller, G.E.; Putnam-Evans, C.; Charbonneau, H.; Ha
Science 252, 951-954, 1991
A:Title: A calcium-dependent protein kinase with a regulatory domain similar to calmo

A:Reference number: A43713; MUID:91240279; PMID:1852075

A:Accession: A43713

A:Molecule type: mRNA

A:Residues: 1-508 <HAR>

C:Superfamily: EMBL:M64987; NID:g169930; PID:RAB00806.1; PID:g169931

C:Keywords: ATP; calcium binding; EF hand; phosphotransferase; serine/threonine-specific

F:32-292/Domain: protein kinase ATP-binding motif

F:40-48/Region: protein kinase ATP-binding motif

F:335-367/Domain: calmodulin repeat homology <EF1>

F:371-403/Domain: calmodulin repeat homology <EF2>

F:407-439/Domain: calmodulin repeat homology <EF3>

F:441-473/Domain: calmodulin repeat homology <EF4>

F:63/Active site: Lys #status predicted

Query Match 75.0%; Score 1944; DB 1; Length 508;

Best Local Similarity 77.7%; Pred. No. 1.6e-65;

Matches 370; Conservative 51; Mismatches 51; Indels 4; Gaps 3;

QY 14 VLPYOTPLRDHYLLGKLGQOGFTTYLCTEKSSTANTACKSIPKRLKVCREDYEDVWR 73

Db 22 VLPQRTQIRVEYVGRKLGQOGFTTCTTRASGKFAKSIKPKRLCKEDYEDVWR 81

QY 74 EIQIMHLSHPNVRIKGTIEDSVFVHVMVECEGELFDRIYSGHSEAEVAKLIKT 133

Db 82 EIQIMHLSHPNVRIKGTIEDSVFVHVMVECEGELFDRIYSGHSEAEVAKLIKT 141

QY 134 ILGVVEACHSLGVMDHDKPENFLDSPKDDAKLKDTPGLSVFYKPGQYLDVVGSPYY 193

Db 142 IVEVVEACHSLGVMDHDKPENFLDSPKDDAKLKDTPGLSVFYKPGSEFCDVVGSPYY 201

QY 194 VAPEVLKCYGPEIDVWSAGVLYLLSGVPPFWAETSGIFRQILQKLDKSPWPTI 253

Db 202 VAPEVLKCYGPEIDVWSAGVLYLLSGVPPFWAETSGIFRQILQKLDKSPWPTI 261

QY 254 SPAADLIYKMLERSPKRISAEALCHPWIVDEQAAPDKPLDPAVLSRLKQFSOMNKT 313

Db 262 SDSAKDLIRKMLDQPKRLTAHEVLRHPWIYDDNAPDKPLDSAVLSRLKQFSAMNKL 321

QY 314 KVALVIAERLSEEEIGGLKELFKMIDTNSGTITFEELKAGLRVGSSELSKSLMD 373

Db 322 KVALVIAERLSEEEIGGLKELFKMIDTNSGTITFEELKAGLRVGSSELSKSLMD 381

QY 374 RADINDSGTIDYGEFLAATLHMKWEREELVAASDFDKDGSYITIDELQSACTEGL 433

Db 382 RADINDSGTIDYGEFLAATLHMKWEREELVAASDFDKDGSYITIDELQSACTEGL 441

QY 434 CDTPLDDMIKEIDLNDGKIDFSEPTAMMRKGD-GVGRSRMTMMKLNENIADAFV 488

Db 442 DDHIEDDMKEIDLNDGKIDFSEPTAMMRKGD-GVGRSRMTMMKLNENIADAFV 494

RESULT 5

S71776

calcium-dependent protein kinase (EC 2.7.1.1) 9 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 18-Jun-1999

C:Accession: S71776; S71775; S71902; S71196

R:Hong, Y.; Takano, M.; Liu, C.M.; Gasch, A.; Chye, M.L.; Chua, N.H.

Plant Mol. Biol. 30, 1259-1275, 1996

A:Title: Expression of three members of the calcium-dependent protein kinase gene family

A:Reference number: S71774; MUID:96311013; PMID:8704134

A:Accession: S71776

A>Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-490 <HON>

A:Cross-references: EMBL:U20626

A:Accession: S71775

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-490 <HOF>

A:Cross-references: EMBL:U20388

R:Hong, Y.; Takano, M.; Liu, C.M.; Gasch, A.; Chye, M.L.; Tan, C.T.; Koh, C.C.; Chua, N.

submitted to the EMBL Data Library, February 1995

A:Description: Expression of the calcium-dependent protein kinase gene family in Arab

A:Reference number: S71197

A:Accession: S71902

A:Molecule type: DNA

A:Residues: 1-164, 'S', '166-239, 'E', '241-300, 'KF', '303-350, 'S', '352-490 <HOW>

A:Cross-references: EMBL:U20626; NID:g836945; PID:AAA67657.1; PID:g836946

R:Hong, Y.; Takano, M.; Liu, C.M.; Gasch, A.; Chye, M.L.; Tan, C.T.; Koh, C.C.; Chua

submitted to the EMBL Data Library, January 1995

A:Description: Expression of the calcium dependent protein kinase gene family in Arab

A:Reference number: S71196

A:Accession: S71196

A:Molecule type: mRNA

A:Residues: 1-164, 'S', '166-239, 'E', '241-300, 'KF', '303-350, 'S', '352-490 <HOA>

A:Cross-references: EMBL:U20388; NID:g836937; PID:AAA67653.1; PID:g836938

C:Genetics:

A:Gene: CDPK9

A:Introns: 177/1; 225/1; 276/1; 370/3; 445/3

C:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein

C:Keywords: ATP; calcium binding; EF hand; phosphotransferase; serine/threonine-spec

F:20-280/Domain: protein kinase homology <KIN>

F:28-36/Region: protein kinase ATP-binding motif

F:323-355/Domain: calmodulin repeat homology <EF1>

F:359-391/Domain: calmodulin repeat homology <EF2>

F:395-427/Domain: calmodulin repeat homology <EF3>

F:429-461/Domain: calmodulin repeat homology <EF4>

F:51/Active site: Lys #status predicted

Query Match 71.2%; Score 1847.5; DB 1; Length 490;

Best Local Similarity 73.5%; Pred. No. 5.6e-62;

Matches 355; Conservative 52; Mismatches 69; Indels 7; Gaps 2;

QY 1 MTKPNRPSNTVLPYOTPLRDHYLLGKLGQOGFTTYLCTEKSSTANTACKSIPK 60

Db 1 MANKPRTR----WVLPYKTKNVEDNFIQVLCGQOGFTTCTKQTKLACKSIPK 56

QY 61 KLVCREDEYVWREIQIMHLSHPNVRIKGTIEDSVFVHVMVECEGELFDRIYSGK 120

Db 57 KLLCQEDYDDVLRREIQIMHLSHPNVRIKGTIEDSVFVHVMVECEGELFDRIYSGK 116

QY 121 HFSREAVKLIKTILGVVEACHSLGVMDHDKPENFLDSPKDDAKLKDTPGLSVFYK 180

Db 117 HYSEREAAKLIKTIVGVVEACHSLGVMDHDKPENFLDSPKDDAKLKDTPGLSVFYK 176

QY 181 GOYLDVWGVSPYVVAPEVLKCYGPEIDVWSAGVLYLLSGVPPFWAETSGIFRQILQ 240

Db 177 GEAFSELVGSAYVVAPEVLKCYGPEIDVWSAGVLYLLSGVPPFWAETSGIFRQILQ 236

QY 241 GKLDPKSDPWTITSEAAKDLIYKMLERSPKRISAEALCHPWIVDEQAAPDKPLDPAVL 300

Db 237 GKLDPEINPWPSPSSAKDLIKKMLSPKRLTAHQVLCHPWIVDDKVPKPLDCAV 296

QY 301 SRLKQFSOMNKTIKKVALVIAERLSEEEIGGLKELFKMIDTNSGTITFEELKAGLRV 360

Db 297 SRLKNGSAMNKKVALVIAERLSEEEIGGLKELFKMIDTNSGTITFEELKAGLRV 356

QY 361 SELMESEIKSLMDAADIDNSGTIDYGEFLAATLHMKWEREELVAASDFDKDGSYIT 420

Db 357 SELMESEIQELLRAADVDESITIDYGEFLAATLHMKWEREELVAASDFDKDGSYIT 416

QY 421 IDELOSACTEGLCDTPLDDMIKEIDLNDGKIDFSEPTAMMRKGDGVGRS---RTMK 477

Db 417 IEELQQAQWKEFGINDSLMDIKDIDQNDQIDYGEFVAMMRKNGTGGGIGRRTMRS 476

QY 478 LNF 480

Db 477 LNF 479

RESULT 6

T03271

calcium-dependent protein kinase (EC 2.7.1.1) 1 - maize

C:Species: Zea mays (maize)

F:464-496/Domain: calmodulin repeat homology <EF3>
F:498-530/Domain: calmodulin repeat homology <EF4>
F:120/Active site: Lys #status predicted

Query Match 67.3%; Score 1745; DB 1; Length 554;
Best Local Similarity 70.0%; Pred. No. 3.8e-58;
Matches 333; Conservative 57; Mismatches 84; Indels 2; Gaps 2;

QY 13 TVLPVOTPLRDLHYLLGKKGQGFQGTTLCTEKSTSANYSACKSIPKRLKLVREDYVW 72
DB 78 SYLGHPTPLRDLALGRKLGQGFQGTTLCTELATGVDYACKSISKRKLITREDVDVR 137
QY 73 REIQIMHLSHPNVRIKGTVEDSVFVHIVMEVCEGGELEFRIYKSGHFSER 132
DB 138 REIQIMHLSGHTNVVAIKGAYEDQLYHIVMELCAGGELFDRIIRGHYSERKAEALTR 197
QY 133 TILGVVEACHSLGVMRDLKPNFLFDSPPKDDAKLKATDFGLSVFYKPGQYLYDVVGSY 192
DB 198 IIVGVVEACHSLGVMRDLKPNFLVNVKDDLSLKAIDFGLSVFYKPGQVTFDVVGSY 257
QY 193 YVAPVVKCYGPEIDVWSAGVILYLLSGVPPFNAETESGIFRQILQKLDKFSDPWPT 252
DB 258 YVAPVLLKNGYPAADVMTAGVILYLLSGVPPFNAETQGGIFDAVLKGVDFDSDPWPV 317
QY 253 ISEAAKDLIYKMLERSPKKRISAEHALCHPWIVDQAPDKPLDPAVLSRLKQFSOMNKL 312
DB 318 ISDSAKDLIRMLNPRSAERLTAHEVLCHPWIRDHGVAPDRPLDPAVLSRIKQFSAMNKL 377
QY 313 KKMALVIAERLSEIEIGLKFEMIDTNSGTTTFEELKAGLRVGSSELSKLSM 372
DB 378 KKMALVIAERLSEIEIGLKFEMIDTNSGTTTFEELKAGLRVGSSELSKLSM 437
QY 373 DAADIDNSGTYGFEALATLHMNMKEREIILVAAPSDPKDGSYITIDELQSACTEFG 432
DB 438 DAADIDNSGTYGFEALATLHMNMKEREIILVAAPSDPKDGSYITIDELQSACTEFG 497
QY 433 LCDTFLDDMIKEIDNDGKIDFSEFTAMMRKGD-GVGRSRTMMKNLNFNIADAFG 487
DB 498 MPDAFLDDVINEADQNDGRIDYGEFVAMTKGNMGVGR-RTMRSLNLSMRDAPG 552

RESULT 9
T06126
calcium-dependent protein kinase (EC 2.7.1.1-) CPK5 - Arabidopsis thaliana
N:Alternate names: protein F23E12.130
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 21-Jan-2000
C:Accession: T06126
R:Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Hoheisel, submitted to the Protein Sequence Database, April 1999
A:Reference number: 215495
A:Accession: T06126
A:Molecule type: DNA
A:Residues: 1-556 <BE>
A:Cross-references: EMBL:AL022604; GSPDB:GN00062; ATSP:F23E12.130
F:434-466/Domain: calmodulin repeat homology <EF2>
F:470-502/Domain: calmodulin repeat homology <EF3>
F:504-536/Domain: calmodulin repeat homology <EF4>

Query Match 67.2%; Score 1742; DB 2; Length 556;
Best Local Similarity 68.4%; Pred. No. 4.9e-58;
Matches 329; Conservative 66; Mismatches 84; Indels 2; Gaps 2;

QY 6 NRPSPNTVLPYQTPRLRDHLLGKKGQGFQGTTLCTEKSTSANYSACKSIPKRLKLCR 65

DB 77 NPDNQAYVYLGHKTPNIRDIYTLISRLKGQGFQGTTLCTEIASGVYACKSISKRKLISK 136
QY 66 EDYEDVWREIQIMHLSHPNVRIKGTVEDSVFVHIVMEVCEGGELEFRIYKSGHFSER 125
DB 137 EDYEDVWREIQIMHLSHPNVRIKGTVEDSVFVHIVMEVCEGGELEFRIYKSGHFSER 196
QY 126 EAVKLITKILGVVEACHSLGVMRDLKPNFLFDSPPKDDAKLKATDFGLSVFYKPGQYLY 185
DB 197 KAAELTKIIVGVVEACHSLGVMRDLKPNFLVNVKDDLSLKAIDFGLSVFYKPGQIET 256
QY 186 DVVGSPIYVAPVVKCYGPEIDVWSAGVILYLLSGVPPFNAETESGIFRQILQKLDK 245
DB 257 DVVGSPIYVAPVVKCYGPEIDVWSAGVILYLLSGVPPFNAETESGIFRQILQKLDK 316
QY 246 KSDPPTISEAAKDLIYKMLERSPKKRISAEHALCHPWIVDQAPDKPLDPAVLSRLKQ 305
DB 317 ESDPFPVSDSARDLIRMLNPRSAERLTAHEVLCHPWIRDHGVAPDRPLDPAVLSRLKQ 376
QY 306 FSQMNKIKKMALVIAERLSEIEIGLKFEMIDTNSGTTTFEELKAGLRVGSSELSME 365
DB 377 FSAMNKLKMALVIAERLSEIEIGLKFEMIDTNSGTTTFEELKAGLRVGSSELSME 436
QY 366 SEIKSLMDAADIDNSGTYGFEALATLHMNMKEREIILVAAPSDPKDGSYITIDELQ 425
DB 437 TEIHLMDAADIDNSGTYGFEALATLHMNMKEREIILVAAPSDPKDGSYITIDELQ 496
QY 426 SACTEFGLCDTFLDDMIKEIDNDGKIDFSEFTAMMRKGD-GVGRSRTMMKNLNFNIAD 484
DB 497 QACVEHGMADVLELDIIEVDQNDGKIDYGEFVEMQKGNAGVGR-RTMRSLNLSMRD 555
QY 485 A 485
DB 556 A 556

RESULT 10
D84550
probable calmodulin-domain protein kinase CPK6 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Mar-2001
C:Accession: D84550
R:Llin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanNaken, S.E.; Umayam, L.; Tallon euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Vente Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: D84550
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-544 <STO>
A:Cross-references: GB:AE002093; NID:g2623752; PIDN:AA886506.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g17290
A:Map position: 2
C:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein C:keywords: EF hand

Query Match 66.8%; Score 1731; DB 2; Length 544;
Best Local Similarity 68.3%; Pred. No. 1.2e-57;
Matches 328; Conservative 65; Mismatches 85; Indels 2; Gaps 2;

QY 6 NRPSPNTVLPYQTPRLRDHLLGKKGQGFQGTTLCTEKSTSANYSACKSIPKRLKLCR 65
DB 65 NVNDGSYYVVLGHKTPNIRDLITSLRKLGQGFQGTTLCTDIATGVYACKSISKRKLISK 124
QY 66 EDYEDVWREIQIMHLSHPNVRIKGTVEDSVFVHIVMEVCEGGELEFRIYKSGHFSER 125
DB 125 EDYEDVWREIQIMHLSHPNVRIKGTVEDSVFVHIVMEVCEGGELEFRIYKSGHFSER 184
QY 126 EAVKLITKILGVVEACHSLGVMRDLKPNFLFDSPPKDDAKLKATDFGLSVFYKPGQYLY 185

Db 185 KAELTKIIVGVVEACHSLGVNHRDLKPNFTLLVKNDDDFSLKATDFGLSVFFKFGQIFK 244
 QY 186 DVVGSPIYVAPVLLKCKYGEIDVWSAGVILYILSGVPPFWAETESGIFRQIOGLKDF 245
 Db 245 DVVGSPIYVAPVLLKHYGPEADVMTAGVILYILSGVPPFWAETQGGIFDAVLKGYIDF 304
 QY 246 KSDPWTITISAAKDLILYKMLERSPKKRISAEALCHPWIVDQOAPDKPLDPAVLSRLKQ 305
 Db 305 DTDPPVLSDSAKDLIRKMLCSPSERLTAHEVLRHPWICENGVPADRALDPVLSRLKQ 364
 QY 306 FQOMNKKKMLARVIAERLSEIEGGLKELFKMIDTNSGTTTFBELKAGLRKRVSELM 365
 Db 365 FQAMNKKKMLKVAESLSEIEAGLRAMFEAMTDNSGTTTFBELKAGLRKRVSELM 424
 QY 366 SEIKSLMDAADTNSGTTIDYGFELAAATHMKNKMEREEILVAFSDFDKDGSYITIDELQ 425
 Db 425 TEIRDMEAADVNSGTTIDYSEFIAATHLNLKEREELVSAFYDFDKDGSYITIDELQ 484
 QY 426 SACTEFGLCDTPLDMDIKEIDLNDGKIDFSEFTAMRKGD-GVGRSRTMMKNLNFNIAD 484
 Db 485 QSCIEHGMDVLEDLIKEVDQDNGRIDYEEFVAMQKGNAGVR-RTMKNLSLISMRD 543
 RESULT 11
 A49082
 calcium-dependent protein kinase (EC 2.7.1.1-) AK1 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 14-May-1998 #sequence_revision 14-May-1999 #text_change 11-Jun-1999
 C:Accession: A49082
 R:Harper, J.F.; Binder, B.M.; Sussman, M.R.
 Biochemistry 32, 3282-3290, 1993
 A:Title: Calcium and lipid regulation of an Arabidopsis protein kinase expressed in Esch
 A:Reference number: A49082; MUID:93213795; PMID:7916621
 A:Contents: ecotype Columbia
 A:Accession: A49082
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-610 <HAR>
 A:Cross-references: GB:L14771; NID:q289189; PIDN:AAA32761.1; PID:g304105
 A:Note: sequence extracted from NCBI backbone (NCBIN:128903, NCBI:P128904)
 C:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kin
 C:Keywords: ATP; calcium binding; EF hand; phosphotransferase; serine/threonine-specific
 F:148-408/Domain: protein kinase homology <KIN>
 F:156-164/Region: protein kinase ATP-binding motif
 F:451-483/Domain: calmodulin repeat homology <EF1>
 F:487-519/Domain: calmodulin repeat homology <EF2>
 F:523-555/Domain: calmodulin repeat homology <EF3>
 F:557-589/Domain: calmodulin repeat homology <EF4>
 F:179/Active site: Lys #status predicted

Query Match 66.5%; Score 1724; DB 1; Length 610;
 Best Local Similarity 65.5%; Pred. No. 2.5e-57;
 Matches 329; Conservative 62; Mismatches 91; Indels 20; Gaps 2;

QY 2 ETKP-----NPRP-----SNTVLPYQTPRDRDHYLLGKKGQGGFGTTY 41
 Db 106 ETKPESKDPAPKPKPKHMKRVSSAGLRSTESVLQRTKNEFEYSGLRKLQGGFGTTF 165
 QY 42 LCTEKSTSAVACKSIPKRLVCREDEDVWREIQIMHLSHPNNVRLKGYEDVSFVH 101
 Db 166 LCVEKITKEFACKIARKKLTDDEVDVRRREIQIMHLAGHPNVISIKGAYEDVAVH 225
 QY 102 IYMEVCEGELPDRIVSKGHFSEREAVKLIKTILGVVEACHSLGVNHRDLKPNELFDS 161
 Db 226 IYMECCAGGELFDRILQIRGHYTERKAAELTRIVGVVEACHSLGVNHRDLKPNELFVSK 285
 QY 162 KDAKLKATDFGLSVFYKPGQYLDVWGSPIYVAPVLLKCKYGEIDVWSAGVILYILS 221
 Db 286 HEDSLKKTIDFGLSMFFKPDVFTDVWGSPIYVAPVLLKCKYGEIDVWSAGVILYILS 345
 QY 222 GYPFWAETESGIFRQIOGLKDFKSDPWTITISAAKDLILYKMLERSPKKRISAEALCH 281
 Db 346 GYPFWAETEQGIFRQVGLHGLDFSSDPWPSISAKDLVRKMLVRDPKRLTATAHQVL 405

QY 282 PWIVDQOAPDKPLDPVLSRLKQFSQMNKIKKMLARVIAERLSSEIEGGLKELFKMIDT 341
 Db 406 PWVQVDGVPADPLDSAVLSRLKQFSAMNKKKMLARVIAESLSEIEAGLKEFMENMIDA 465
 QY 342 DNSGTTITFEELKAGLRKRVSELMSEIEKSLMDAADTNSGTTIDYGFELAAATHMKNKMER 401
 Db 466 DKSQGITFEELKAGLRKRVGANLKESEIIDLMOAADVNSGTTIDYKEFTAAATHLKNKIERE 525
 QY 402 EILVAAFDFDKDGSYITIDELQACTEFGLCDTPLDMDIKEIDLNDGKIDFSEFTAM 461
 Db 526 DHLFAFTYFDKDGSIYITPELQACQEEFGVEDVRIELMRDVPDQDNGRIDYNEFYAM 585
 QY 462 MRKGDGVRGSRRTMMKNLNFNIA 483
 Db 586 MOKGSITGTPVKMGLKSFSA 607
 RESULT 12
 T09940
 calcium-dependent protein kinase (EC 2.7.1.1-) CDPK - pumpkin
 N:Alternate names: calcium-dependent calmodulin-independent protein kinase CDPK
 C:Species: Cucurbita pepo (pumpkin)
 C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
 C:Accession: T09940
 R:Ellard-Ivey, M.; Hopkins, R.B.; White, T.J.; Lomax, T.L.
 Plant Mol. Biol. 39, 199-208, 1999
 A:Title: Cloning, expression and N-terminal myristoylation of CcpPK1, a calcium-depen
 A:Reference number: 216898; MUID:99178773; PMID:10080688
 A:Accession: T09940
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-573 <ELL>
 A:Cross-references: EMBL:U90262; NID:gl899174; PIDN:AAB49984.1; PID:gl899175
 A:Experimental source: etiolated hypocotyls
 C:Genetics: CPK1
 C:Gene: CPK1
 C:Function:
 A:Description: serine/threonine-specific protein kinase activated by direct binding c
 C:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein
 C:Keywords: ATP; calcium binding; EF hand; membrane protein; myristylation; phosphot
 F:108-368/Domain: protein kinase homology <KIN>
 F:447-479/Domain: calmodulin repeat homology <EFH>

Query Match 65.9%; Score 1709.5; DB 2; Length 573;
 Best Local Similarity 64.8%; Pred. No. 8e-57;
 Matches 321; Conservative 78; Mismatches 79; Indels 17; Gaps 3;

QY 4 KPNRP-----RP-----SNTVLPYQTPRLRDHYLLGKKGQGGFGTTYLCTEKS 47
 Db 72 KPEPPMEPKVRPMKRVSGAGLRGGSVLQTKTGNFKFKEYSLGKKGQGGFGTTYMCVEKA 131
 QY 48 TSANYACKSIPKRLVCREDEDVWREIQIMHLSHPNNVRLKGYEDVSFVHIVMEVC 107
 Db 132 TGKEYACKSIARKLVNEDDVEDVRRREIQIMHLSGHPNVISIKGAYEDAVAVQVVMELC 191
 QY 108 EGGEFLDRIVKSGHFSEREAVKLIKTILGVVEACHSLGVNHRDLKPNELFDSPKDDAKL 167
 Db 192 AGGELFDRILQIRGHYTERKAAELTRIVGVVEACHSLGVNHRDLKPNELFVFSKEESLL 251
 QY 168 KATDFGLSVFYKPGQYLDVWGSPIYVAPVLLKCKYGEIDVWSAGVILYILSGVPPFW 227
 Db 252 KTFIDGLSMFFKPGKFNVDVWGSPIYVAPVLLKCKYGEADVWSAGVILYILSGVPPFW 311
 QY 228 AETESGIFRQIOGLKDFKSDPWTITISAAKDLILYKMLERSPKKRISAEALCHPWIV 287
 Db 312 AESERGIEEVLHGLDFSSDPWPSISAKDLVRMLVRDPKRLTAYEVLCHPWVQVD 371
 QY 288 QAAPKPLDPVLSRLKQFSQMNKIKKMLARVIAERLSSEIEGGLKELFKMIDTNSGTI 347
 Db 372 GVADPKPLDSAVLTRELKQFSAMNKKKMLARVIAESLSEIEAGLKEFMKIDTNSQGI 431
 QY 348 TFEELKAGLRKRVSELMSEIEKSLMDAADTNSGTTIDYGFELAAATHMKNKMEREEILVAA 407

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Db      432  TPEELKAGLKKFGANLKESIEYDLMOQAADIDNNGTTIDYGFEVAAATLHLNKIKEDHLLAA 491
QY      408  FDSFDXDGSGYITIDEQLSACTEFFGGLCDPLDMDIKEIDLNDGNKITDRFSEFTAMMRKG DG 467
Db      492  FSFYDXDGSGFITHDLEQQACKFEGLDELMEEEMKEVDQNNDGSIDYNEFVAMMOKGV 551
QY      468  VGRSRMTMKNLNFNI 482
Db      552  VNTGGKLQS-SFSI 565

RESULT 13
T05650
calcium-dependent protein kinase (EC 2.7.1.1-) F20D10.350 - Arabidopsis tha
N;Alternate names: Protein F20D10.350
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-April-1999 #sequence_revision 23-Apr-1999 #text_change 21-Jan-2000
R;Accession: T05650
R;Bevan, M.; Wedler, H.; Kutzner, M.; Wambutt, R.; Bancroft, I.; Mewes, H.V.
submitted to the Protein Sequence Database, February 1999
A;Reference number: Z15420
A;Accession: T05650
A:Molecule type: DNA
A;Residues: 1-484 <BEV>
A;Cross-references: EMBL:AL035538
A;Experimental source: cultivar Columbia; BAC clone F20D10
C;Genetics:
A;Map position: 4
A;Intons: 179/1; 227/1; 278/1; 316/3; 372/3; 447/3
A;Note: F20D10.350
C;Superfamily: calcium-dependent protein kinase; calmodulin repeat homolog
F;22-282/Domain: protein kinase homology <XIN>
F;30-38/Region: protein kinase ATP-binding motif
F;325-357/Domain: calmodulin repeat homology <EFl>
F;361-393/Domain: calmodulin repeat homology <EF2>
F;397-429/Domain: calmodulin repeat homology <EF3>
F;431-463/Domain: calmodulin repeat homology <EF4>
F;53/Active site: Lys #status predicted
```

```

QY   434 CDTPLDMDIKEIDLNDGKIDFSEFTAMMRKGDSVGRSRTMMKKMLNPNFI 482
      I :|::||::||::||::||::||::||::||::||::||::||::||::|| 
Db    432 SDVFLEDIKEVDQNDRIDIYGFEVAMMQGI-VG--RTMRRKSINMSI 477

RESULT 14
T02784
calcium-dependent protein kinase (EC 2.7.1.1) - maize (strain W64A)
C;Species: Zea mays (maize)
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 16-Jun-2000
C;Accession: T02784
R;Murillo, I.; Jaack, E.; Cordero, M.; San Segundo, B.
submitted to the EMBL Data Library, July 1998
A;Description: A calcium-dependent protein kinase possibly involved in pathogen defen-
sis-related Ptns gene.
A;Reference number: Z14736
A;Accession: T02784
A;Status: translated from GS/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-639 <WUR>
A;Cross-references: EMBL:AJ007366; PIDN:CAA07481.1
A;Experimental source: strain W64A; seed
C;Function:
A;Description: probably involved in pathogen defense in maize plants
C;Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein
C;Keywords: ATP; calcium binding; EF hand; phosphotransferase; serine/threonine-speci-
F;151-411/Domain: protein kinase homology <KIN>
F;159-167/Region: protein kinase ATP-binding motif
F;454-486/Domain: calmodulin repeat homology <EF1>
F;490-522/Domain: calmodulin repeat homology <EF2>
F;526-558/Domain: calmodulin repeat homology <EF3>
F;560-592/Domain: calmodulin repeat homology <EF4>
F;182/Active site: Lys #status predicted

Query Match          64.5%; Score 1672.5; DB 1; Length 639;
Best Local Similarity 66.2%; Pred. No. 2e-55;
Matches 318; Conservative 66; Mismatches 83; Indels 13; Gaps 3;

QY   5 PNPR-RPS-----NTVLPTQPRLRDHYLLCKLKGGOGFYTLCTEKSTSNANY 52
      |||:|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
Db    120 PSPPRPQVRKVSSAGILLGSVLRKKTENKDKYSLSGRIGCGQGFGTHLCVERATKEL 179

QY   53 ACKSIPIRKLVCREDYEDVWRREIQIMHSLSEHPNVVRIKGYEDSVFHVIMEVCEGGE 112
      |||:|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
Db    180 ACKSILKRKLGSDDVEDVRREIQIMHLAGHPSSVGIRGAYEDAVAHVLMELCGGGE 239

QY   113 FDIRTVSGHFSEEREAVKLITILGVACHSLSGMHRDLKPENFLFDSPKDADAKLKATDF 172
      |||:|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
Db    240 FDIRVRGHYTEKAELARIVGVGVACHSMSGVMHRDLKPENLFFADHSEEAAKLTIDF 299

QY   173 GLSVFYKPGOYLXDVNGSPYYVAPEVLKCYGPBIDVWSAGVTLYILLSGVPFPWFATES 232
      |||:|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
Db    300 GLSTIFFPFGQTTFDVGSPYYVAPEVLKRYGPADVWSAGVTIYILLGVPPFWAEANEQ 359

QY   233 GIFPQIILOGLDPKSDSWPTISEAAKDLIVKMFLERSPKKRISAHEALCHPWIDEQAAPD 292
      |||:|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
Db    360 GIFEEVLRHLRDFESEWPQLISDGAKDLVRLMVLPDRPKRLTAHEVLRHPVVQGVGVAPD 419

QY   293 KPLDPVLSRLKFOSMNKKWKALRVIAERLSREEIGGLKELFKMTIDTSNGTIIFEEL 352
      |||:|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
Db    420 RPLDSAVLSRMKQFSANMKLKWALRVIAEINLSDEIAGLRMEFKMIDADNSGOITFEEL 479

QY   353 KAGLKRVSSELMESEIKSLMDAADINSGITDYGFELAATHLNKNWEREBELLVAASDFD 412
      |||:|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
Db    480 KVGLKEYGANLQSEIYIALMAADVDDNNGTIDYGEFTAATHLNKVBREDHLLFAAFQYFD 539

QY   413 KDGSGYTTIDESACTEFGLCDTPDLLDMTKIEDLDNDGKIDFSEFTAMMRKGDSVGRSR 472
      |||:|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
Db    540 KDGSYITADELVACGEFGLDVQLDEGDNDGRIDYNFVAMMQK-PTVGGSR 598

RESULT 15
H84810
```


GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 26, 2003, 11:57:52 ; Search time 22 Seconds

(without alignments)
933.217 Million cell updates/sec

Title: US-09-848-806-1

Perfect score: 2593

Sequence: 1 METKPNRRPSNTVLPYQTP.....KNLNFNIADAFGVGDKSD 495

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1944	75.0	508	1	CDPK_SOYBN
2	1724	66.5	610	1	CDP1_ARATH
3	1586	61.2	542	1	CDP3_ORYSA
4	1482	57.2	533	1	CDP2_ORYSA
5	1460	56.3	513	1	CDP2_MAIZE
6	1460	56.3	534	1	CDP1_ORYSA
7	1432.5	55.2	532	1	CDPK_DAUCA
8	854	32.9	602	1	CRK_DAUCA
9	591	22.8	499	1	KCCD_HUMAN
10	589.5	22.7	374	1	KCC1_RAT
11	587.5	22.7	370	1	KCC1_HUMAN
12	578.5	22.3	473	1	KCC4_HUMAN
13	574.5	22.2	533	1	KCCD_RAT
14	574	22.1	469	1	KCC4_MOUSE
15	572	22.1	474	1	KCC4_RAT
16	571.5	22.0	542	1	KCCB_MOUSE
17	569.5	22.0	542	1	KCCB_RAT
18	567.5	21.9	478	1	KCCA_HUMAN
19	566.5	21.8	664	1	KCCB_HUMAN
20	563.5	21.7	478	1	KCCA_RAT
21	549.5	21.2	478	1	KCCA_MOUSE
22	544.5	21.0	529	1	KCCG_MOUSE
23	543.5	21.0	472	1	KCCG_HUMAN
24	539	20.8	527	1	KCCG_RAT
25	534.5	20.6	424	1	KPSH_HUMAN
26	533.5	20.6	386	1	KPSH_HUMAN
27	532.5	20.5	386	1	KPBG_HUMAN
28	526	20.3	387	1	KPBG_RAT
29	524.5	20.2	387	1	KPBG_MOUSE
30	514.5	19.8	295	1	KMLC_DICDI
31	509	19.6	1431	1	DAPK_HUMAN
32	505	19.5	433	1	DKK1_RAT
33	505	19.5	740	1	DKK1_HUMAN

34	505	19.5	756	1	DKK1_MOUSE
35	499	19.2	335	1	KCC1_SCHPO
36	489.5	18.9	752	1	K6AA_CHICK
37	486	18.7	735	1	K6AL_RAT
38	484.5	18.7	512	1	K110_ARATH
39	482.5	18.6	733	1	K6A2_HUMAN
40	481	18.5	724	1	K6AL_MOUSE
41	480	18.5	735	1	K6AL_HUMAN
42	479	18.5	546	1	CHK2_MOUSE
43	477	18.4	733	1	K6AA_XENLA
44	476.5	18.4	733	1	K6A2_MOUSE
45	476	18.4	543	1	CHK2_HUMAN

ALIGNMENTS

```
RESULT 1
CDPK_SOYBN
ID CDPK_SOYBN STANDARD; PRT; 508 AA.
AC P28583;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Calcium-dependent protein kinase SK5 (EC 2.7.1.1-) (CDPK).
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycyne.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Williams;
RX MEDLINE=91240279; PubMed=1852075;
RA Harper J.F., Sussman M.R., Schaller G.E., Putnam-Evans C.,
RA Charbonneau H., Harmon A.C.;
RT "A calcium-dependent protein kinase with a regulatory domain similar
RT to calmodulin."
RL Science 252:951-954(1991).
CC -!- FUNCTION: MAY PLAY A ROLE IN SIGNAL TRANSDUCTION PATHWAYS THAT
CC INVOLVE CALCIUM AS A SECOND MESSENGER.
CC -!- ENZYME REGULATION: ACTIVATED BY CALCIUM. AUTOPHOSPHORYLATION MAY
CC PLAY AN IMPORTANT ROLE IN THE REGULATION OF THE KINASE ACTIVITY.
CC -!- TISSUE SPECIFICITY: FOUND THROUGHOUT THE PLANT.
CC -!- MISCELLANEOUS: THERE ARE MULTIPLE CDPK ISOFORMS IN SOYBEAN.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CAMK SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
CC EMBL; M64987; AAB00806.1;
CC PIR; A43713; A43713.
CC HSSP; O63450; 1A06.
CC InterPro; IPR000719; Euk_pkinase.
CC InterPro; IPR002048; EF-hand.
CC Pfam; PF00036; ehand; 4.
CC ProDom; PD000001; Euk_pkinase; 1.
CC ProDom; PD000012; EF-hand; 2.
CC SMART; SM00054; S_TKc; 1.
CC SMART; SM00220; EF-hand; 4.
CC PROSITE; PS00018; EF_HAND; 4.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
CC PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
```



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Db 286 HEDSLKTIIDFGLSMFKPDVDTVDVGVSPYYVAPEVLRKRYGPEADVWSAGVIVYLLS 345
QY 222 GVPPFWAETESGIFRLOILOKLFKSDPWPPTISEAAKDLIYKMLERSPKKRISAHEALCH 281
Db 346 GVPPFWAETESGIFRLOILOKLFKSDPWPPTISEAAKDLIYKMLERSPKKRISAHEALCH 405
QY 282 PWTVDQAAADKPLDPAVLRLKQFQSMNKKKMAKLVIAERLSEEEIGGLKELFKMIDT 341
Db 406 PWQVQGVADPKPLDPAVLRLKQFQSMNKKKMAKLVIAERLSEEEIGGLKELFKMIDT 465
QY 342 DNGSTTTFEELKAGLRVGSSELMESEKSLMDAADINDSGTIDYGFELATLHMKNKERE 401
Db 466 DKSGQTFEELKAGLRVGSSELMESEKSLMDAADINDSGTIDYGFELATLHMKNKERE 525
QY 402 EILVAFSPDKDGSYYITIDELQSACTERGLCDTFLDMDIKEDIDNDGKIDFSEFTMA 461
Db 526 DHLEAFAFTYFDKGSYYITIDELQSACTERGLCDTFLDMDIKEDIDNDGKIDFSEFTMA 585
QY 462 MRKGDGVGRSRTMMKNLNFENIA 483
Db 586 MQKSGTIGFVPMGLEKSFSA 607

RESULT 3
CDP3_ORYSA
ID CDP3_ORYSA STANDARD; PRT; 542 AA.
AC P53684;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Calcium-dependent protein kinase, isoform 11 (EC 2.7.1.1-) (CDPK 11).
GN Cpk11.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv Arborio; TISSUE=coleoptile;
RA Breviaro D., Morello L., Giani S.;
RT "Molecular cloning of two novel rice cDNA sequences encoding putative
RL Plant Mol. Biol. 27:953-967(1995).
CC 1- FUNCTION: MAY PLAY A ROLE IN SIGNAL TRANSDUCTION PATHWAYS THAT
CC INVOLVE CALCIUM AS A SECOND MESSENGER.
CC 1- ENZYME REGULATION: ACTIVATED BY CALCIUM (BY SIMILARITY).
CC 1- MISCELLANEOUS: THERE ARE MULTIPLE CDPK ISOFORMS IN RICE.
CC 1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CAMK SUBFAMILY.
CC 1- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS. THREE OF
CC THEM SEEM TO BE NON FUNCTIONAL.

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DR PROSITE; PS00018; EF_HAND; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
KW Transferrase; Serine/threonine-protein kinase; ATP-binding;
KW Calcium-binding; Phosphorylation; Multigene family.
FT DOMAIN 79 337 PROTEIN KINASE.
FT NP_BIND 81 89 ATP (BY SIMILARITY).
FT BINDING 107 107 ATP (BY SIMILARITY).
FT ACT_SITE 202 202 ATP (BY SIMILARITY).
FT DOMAIN 393 404 ANCESTRAL CALCIUM SITE 1 (POTENTIAL).
FT DOMAIN 429 440 ANCESTRAL CALCIUM SITE 2 (POTENTIAL).
FT DOMAIN 465 476 ANCESTRAL CALCIUM SITE 3 (POTENTIAL).
FT CA_BIND 499 510 EF-HAND 4 (POTENTIAL).
SQ SEQUENCE 542 AA; 61166 MW; D4D257275G126DDA CRC64;

Query Match 61.2%; Score 1586; DB 1; Length 542;
Best Local Similarity 63.9%; Pred. No. 1.5e-72;
Matches 304; Conservative 68; Mismatches 102; Indels 2; Gaps 2;

QY 11 SNTVLPVQTPRLRDHYLLGKLGOGFGTTLCTEKTSTANYACKSIPKRLKVCREDYED 70
Db 64 SINVLGRKTADLRHYIIGRLKGQAQFGTTLCTEINCEYACKTIPKRLKITREDVED 123
QY 71 VMREIQIMHLSHPNVRKGTYSVVFHIVMEVCEGSELFDRIVKSGHFSERAEVKL 130
Db 124 VRREIQIMHLSGKNVWAIKDVYEDGQAVHIVMELCAGSELFDRIQEKGHYSERKAAEL 183
QY 131 IKTLGVVEACHSLGVNHRDLKPELFDSPKDDAKLKTDFGLSVFYKPGQYLYDVVGS 190
Db 184 IRIISIVACHSLGVNHRDLKPELFDSPKDDAKLKTDFGLSVFYKPGQYLYDVVGS 243
QY 191 PYVAPEVLKCYGPRIDVWSAGVILYLLSGVPPVPAETESGIFRLOILOKLFKSDPW 250
Db 244 PYVAPEVLKCYGPRIDVWSAGVILYLLSGVPPVPAETESGIFRLOILOKLFKSDPW 303
QY 251 PTISEAAKDLIYKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAVLRLKQFQSMN 310
Db 304 PKISDSAKDLIRKMLSHCPSERLKAHEVLRHFWICENGVAQTQALDPSVISRLKQFSAMN 363
QY 311 KIKKMAKLVIAERLSEEEIGGLKELFKMIDTNSGTITFEELKAGLRVGSSELMESEK 370
Db 364 KUKKIALRVIAERLSEEEIGGLKELFKMIDTNSGTITFEELKAGLRVGSSELMESEK 423
QY 371 LMDAADINDSGTIDYGFELATLHMKNKEREILVAAPSDFKDGSYITIDELQSACTE 430
Db 424 IMEAHNDNNVTIHYEEFIAATLPINKTEREEHLLAAFTYFDKDGSGYITVDKIQORACE 483
QY 431 FGLCDTFLDMDIKEDIDNDGKIDFSEFTAMMRKMGDGVGRS-RTMMKNLNFENIADA 485
Db 484 HNMDLSLEEIISEVDQNDGQIDYAEFVAMN-QGSNVGLGWQTWESSLNVALRDA 538

RESULT 4
CDP2_ORYSA
ID CDP2_ORYSA STANDARD; PRT; 533 AA.
AC P53683;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Calcium-dependent protein kinase, isoform 2 (EC 2.7.1.1-) (CDPK 2).
GN CPK2.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv Arborio; TISSUE=coleoptile;
RA Breviaro D., Morello L., Giani S.;
RT "Molecular cloning of two novel rice
RT calcium-dependent protein kinases.";
RT calcium-dependent protein kinases.";
```



```
SQ SEQUENCE 513 AA; 58081 MW; 235A61630C0AC336 CRC64;
Query Match 56.3%; Score 1460.5; DB 1; Length 513;
Best Local Similarity 60.0%; Pred. No. 2.5e-66;
Matches 276; Conservative 78; Mismatches 105; Indels 1; Gaps 1;

QY 7 PRPSPNTVLPYQTPRLDHYLGLKLGOGQFGTTLCTEKSFSANYACKSIKPKRLVCRE 66
D 46 PPTADTILGKGYEDVRVSYPGKELGRGQFGVTILCTEIASGRQVACKSIKRLVSKA 105
QY 67 DYEDVWREIQIMHHSHPNVRIRKTYEDSDVSVFHVHMEVCEGGELFDRIVSKGHFSERE 126
D 106 DREDIRREIQIMHLSGQPNIVFPRGAYEDKSNVHVWVWELCAGGELFDRILAKGHYTERA 165
QY 127 AVKLTKTILGVVEACHSLGVHMDLKPENFLDPSKDAKLKATQFGLSVFYKQOYLVD 186
D 166 AATICRAVVNVNICHFMGVHMDLKPENFLATMEENAMLKATDFGLSVFYEEGKMVRD 225
QY 187 VVGSPYVAPEVKKCYGPEIDVWSAGVTLXLLSGVPPFWAETESGIFROILOGKLPFK 246
D 226 IVGSAYVAPVIRSYGKEIDVWSAGVILYLLSGVPPFWAETEKGFIDAILHEIDFE 285
QY 247 SDPWTISAAKDLIKMLERSPKKRISAEALCHPWIWDQAAQPKPLDPAVLRLKQF 306
D 286 SQPWSISAKDLVRKMLTRDPKKRLTSAQVLQHWLREGGEASDKPIDSALSRMKQF 345
QY 307 SOMNKKIKMALVIAERLSEEEIGGLKELPKMIDTDSGTTTFEELKAGLKRVGSELMES 366
D 346 RAMNKKIKMALVIAERLSEEEIGGLKELPKMIDTDSGTTTFEELKAGLKRVGSELMES 405
QY 367 EIKSLMDAADINSGTIDYGEFFLAATLHMKWREIIVAAFSDFDKGSGYITIDELOS 426
D 406 EVKOLMEAADVNGSIDYVEFTATMRHLKRLERDEHLFKAFQFDFKNSGFIITRDELES 465
QY 427 ACTFEGLCDT-PLDMDIKELIDNDGKIDFSEFTAMMRKG 465
D 466 ALIEHEMGDTTIREITSEVTDNDGRINYEFCAMMRGG 505

RESULT 6
CDPL_ORYSA STANDARD; PRT; 534 AA.
AC P53682;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Calcium-dependent protein kinase, isoform 1 (EC 2.7.1.-) (CDPK 1).
GN SPK.
OS Oryza sativa (rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzoideae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA MEDLINE=93314961; PubMed=8325505;
RX Kawasaki T., Hayashida N., Baba T., Shinozaki K., Shimada H.;
RT "the gene encoding a calcium-dependent protein kinase located near
RT the sbel gene encoding starch branching enzyme 1 is specifically
RT expressed in developing rice seeds.";
RL Gene 129:183-189(1993).
CC -1- FUNCTION: MAY PLAY A ROLE IN SIGNAL TRANSDUCTION PATHWAYS THAT
CC INVOLVE CALCIUM AS A SECOND MESSENGER.
CC -1- ENZYME REGULATION: ACTIVATED BY CALCIUM (BY SIMILARITY).
CC -1- DEVELOPMENTAL STAGE: SPECIFICALLY EXPRESSED IN SEEDS.
CC -1- MISCELLANEOUS: THERE ARE MULTIPLE CDPK ISOFORMS IN RICE.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CAMK SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS. THREE OF
CC THEM SEEM TO BE NON FUNCTIONAL.
CC -----
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CC -----
DR EMBL; D13436; BAA02698.1; -.
DR HSSP; P02593; ICDM.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00036; ehand; 4.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 1.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 2.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00018; EF_HAND; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR Transer; Serine/threonine-protein kinase; ATP-binding;
KW Calcium-binding; Phosphorylation; Multigene family.
FT DOMAIN 73 331 PROTEIN KINASE.
FT NP_BIND 79 87 ATP (BY SIMILARITY).
FT BINDING 102 102 ATP (BY SIMILARITY).
FT ACT_SITE 197 197 BY SIMILARITY.
FT DOMAIN 387 398 ANCESTRAL CALCIUM SITE 1 (POTENTIAL).
FT DOMAIN 422 432 ANCESTRAL CALCIUM SITE 2 (POTENTIAL).
FT DOMAIN 457 468 ANCESTRAL CALCIUM SITE 3 (POTENTIAL).
FT CA_BIND 491 502 EF-HAND 4 (POTENTIAL).
SQ SEQUENCE 534 AA; 60573 MW; 1932CD2C4F8FC85 CRC64;

Query Match 56.3%; Score 1460; DB 1; Length 534;
Best Local Similarity 59.2%; Pred. No. 2.8e-66;
Matches 280; Conservative 84; Mismatches 105; Indels 4; Gaps 4;

QY 14 VLPYQTPRLRDHYLGLKLGOGQFGTTLCTEKSFSANYACKSIKPKRLVCREDDYVWR 73
D 61 VLGYKTPNVRRELYTLGRELGGOGFGKTYLCTEISTGCOYACKTILKSNLRCVSDIEDVRR 120
QY 74 EIQIMHLSHPNVRIRKTYEDSDVSVFHVHMEVCEGGELFDRIVSKGHFSEREAVKLTK 133
D 121 EIQIMHLSGQKNIVTITKDYEDQAVHIVMELCAGGELFSKIQKRGHYSERKAAELIKI 180
QY 134 ILGVVEACHSLGVHMDLKPENFLDPSKDAKLKATDFGLSVFYKQOYLVDVVGSPY 193
D 181 IVGIIFCHSHGVHMDLKPENFLDPSKDAKLKATDFGLSVFYKQOYLVDVVGSPY 240
QY 194 VAPEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETESGIFROILOGKIDFSDPWPPTI 253
D 241 IAPVLEKRYGPEADITWAGVILYLLTGVPPFWADTQSGIYKVLGDRIDFKSNRPRI 300
QY 254 SEAKDLIKMLERSPKKRISAEALCHPWIWDQAAQPKPLDPAVLRLKQFSQMKIK 313
D 301 SDSAKDLIKMLCYPPLERLKAHEVLKHPWTCNGVATNRALDPSVLPRLKQFSAMNRLK 360
QY 314 KMALVIAERLSEEEIGGLKELPKMIDTDSGTTTFEELKAGLKRVGSELMESIKSLMD 373
D 361 KLSLOIARLSEEEIVGLREMFAMKMTKRSVVTFGELK-GUKRYSVFKDEINDLME 419
QY 374 AADINDSGTIDYGEFFLAATLHMKWREIIVAAFSDFDKGSGYITIDELOSACTEFG 433
D 420 AAD-DTTSTINWEEFIAAAYSLNKBREKHLMAFTYDFDKGSGFITVDLQKACMERNM 478
QY 434 CDPPLDMDIKELIDNDGKIDFSEFTAMMRKG-DVGRSRMTMKNLNFNTADA 485
D 479 EDTFLEEMILEVDQNDGQIDYAFVMTMQSNFNLG-WQTVESLNLVALRE 530

RESULT 7
CDPK_DAUCA
```


DR SMART: SM00220: S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
FT Repeat.
FT DOMAIN 20 40 3 X 7 AA TANDEM REPEATS OF S-[LI]-P-X-X-
D-X.
FT REPEAT 20 26 1.
FT REPEAT 27 33 2.
FT REPEAT 34 40 3.
FT DOMAIN 148 410. PROTEIN KINASE.
FT NP_BIND 154 162. ATP (BY SIMILARITY).
FT BINDING 180 180. ATP (BY SIMILARITY).
FT ACT_SITE 276 276. BY SIMILARITY.
FT DOMAIN 465 476. ANCESTRAL CALCIUM SITE 1 (POTENTIAL).
FT DOMAIN 502 513. ANCESTRAL CALCIUM SITE 2 (POTENTIAL).
FT DOMAIN 542 553. ANCESTRAL CALCIUM SITE 3 (POTENTIAL).
FT DOMAIN 574 585. ANCESTRAL CALCIUM SITE 4 (POTENTIAL).
SQ SEQUENCE 602 AA; 67184 MW; 1D10BF68B37BF447 CRC64;
Query Match 32.9%; Score 854; DB 1; Length 602;
Best Local Similarity 41.2%; Pred. No. 5, 1e-36;
Matches 184; Conservative 90; Mismatches 155; Indels 18; Gaps 8;
QY 28 LSKKLGGQFGTYLCTEKSTSYANY-----ACKSTPKKLVCREDEDYEDVWREIQIMHLS 82
Db 150 VGEVGRGHFG--YTCRAKFKGEGKGDVAVKVPKAMITAIADVVRREVVKILRALT 207
QY 83 EHPNVVRIRKGTVEDSVFHVMEVCEGELFDRIYSK-GHSESEAVKLITILGVVEAC 141
Db 208 GHNLVQVYDAFEDHTNVVMECEGELLDRILSRGKGYTDDAKVMQIILNVAF 267
QY 142 HSLGVWHRLDLPENLFDPSDKLAKTDFGLSVFYKPGQVLYDVGVSPYVAPEVLKK 201
Db 268 HLQGVVHRLDLPENLFLSKSDSOLKAIDFGLSDYVVKPDLNLDIVGSAYYVAPEVLHR 327
QY 202 CYGPIDVWSAGVILYIILLGVPVPWATESIFRQILQGLDKFSDWPITSEAKDLI 261
Db 328 SYSTADVWSIGVSYIILLGSRPFWATESIFRAVILKANLSDFPDPWPVSSSEAKDFV 387
QY 262 YKMLERSPKKRISAHEALCHPWIVDEQAAPKPLDPAVLSRLKQFSQMNKKKMLALRTA 321
Db 388 KRLLNKDKRMTAAQAALCHSWIKNSNDI-KFPLDILVFLKMKVYRSPLEKALRAL 446
QY 322 EELSSEETGGLKELFKMIDTDSNGTITTEELKAGLKRVGSELM-ESEIKSLMDAADIDNS 380
Db 447 KTLTVDFELFKELQEVLEPTKNGTISLENIKQALMRNSTAMKDSRVLDLILVSLNALQY 506
QY 381 GTIDYGEFLAATLHMKNMER----EELVAAFSDFDKDGSVITIDELQSACTERGLCDT 436
Db 507 RMDQFEFCAALSVHQLEALDRWEQHARCAVDLEFKDGNRAIMTEELAS---ELGLGFS 563
QY 437 -PLDMIKIEIDLNDGKIDFSEFTAMM 462
Db 564 IPVHAVLHDWIRHTDGLKSLFLGYVKLL 590

RESULT 9

KCCD_HUMAN STANDARD; PRT; 499 AA.
AC Q13557; Q9UQE9; Q9UGH6;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Calcium/calmodulin-dependent protein kinase type II delta chain (EC 2.7.1.123) (Cam-kinase II delta chain) (Cam kinase II delta subunit) (CaMK-II delta subunit).
DE (CaMK-II delta subunit).
GN CAMK2D.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;

RN [1] SEQUENCE FROM N.A.
RP TISSUE-Myocardium;
RX MEDLINE=99205154; PubMed=10189359;
RA Hoch B., Meyer R., Hettler R., Krause E.-G., Karczewski P.;
RT "Identification and expression of delta-isoforms of the
RT multifunctional Ca2+/calmodulin-dependent protein kinase in failing
RT and nonfailing human myocardium.";
RL Circ. Res. 84:713-721(1999).
RN [2]
RP SEQUENCE OF 1-243 FROM N.A.
RC TISSUE-Insulinoma;
RA Rochlitz H., Voigt A., Lankat-Buttgereit B., Goetze B., Heimberg H.,
RA Nauck M.A., Schiemann U., Schatz H., Pfeiffer A.;
RT "Cloning of the human calcium/calmodulin dependent protein kinase II
RT isoforms in human beta cells.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 302-417 FROM N.A.
RX MEDLINE=97214519; PubMed=9060999;
RA Tombes R.M., Krystal G.W.;
RT "Identification of novel human tumor cell-specific CaMK-II variants.";
RL Biochim. Biophys. Acta 1355:281-292(1997).
CC -!- FUNCTION: THIS KINASE MAY PLAY A ROLE IN NEUROTRANSMISSION.
CC -!- CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.
CC -!- ENZYME REGULATION: AUTOPHOSPHORYLATION OF CAM-KINASE II PLAYS AN
CC IMPORTANT ROLE IN THE REGULATION OF THE KINASE ACTIVITY.
CC -!- SUBUNIT: COMPOSED OF FOUR DIFFERENT CHAINS: ALPHA, BETA, GAMMA,
CC AND DELTA.
CC -!- ALTERNATIVE PRODUCTS: 4 ISOFORMS: DELTA 1, DELTA 2 (SHOWN HERE),
CC DELTA 3, DELTA 4, DELTA 8, DELTA 9; ARE PRODUCED BY ALTERNATIVE
CC SPLICING.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN CARDIAC MUSCLE AND SKELETAL
CC MUSCLE.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CAMK SUBFAMILY.

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EMBL; AF071569; AAD20442.1; -
EMBL; AJ252239; CAB65123.1; -
EMBL; U50361; AAB16866.1; -
HSSP; Q63450; 1A06 CAMK2D.
Genew; HGNC:1462; CAMK2D.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
Pfam; PF00069; pkinase; 1.
ProDom; PD000001; Euk_pkinase; 1.
SMART; SM00220; S_TKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
KW Transferase; Serine/threonine-protein kinase; Calmodulin-binding;
KW Phosphorylation; ATP-binding; Neurone; Alternative splicing.
FT DOMAIN 14 272. PROTEIN KINASE.
FT NP_BIND 20 28. ATP (BY SIMILARITY).
FT BINDING 43 43. ATP (BY SIMILARITY).
FT ACT_SITE 136 136. BY SIMILARITY.
FT DOMAIN 291 301. CALMODULIN-BINDING (BY SIMILARITY).
FT CONFLICT 39 39. G->E (IN REF. 2).
SQ SEQUENCE 499 AA; 56297 MW; BBEF05669A883E55 CRC64;

Query Match 22.8%; Score 591; DB 1; Length 499;
Best Local Similarity 37.1%; Pred. No. 5, 4e-23;
Matches 142; Conservative 65; Mismatches 144; Indels 32; Gaps 9;

QY 21 RLDRHYLLGKLGQFGTYLCTEKSTSYANYACKSTPKKLVCREDEDYEDVWREIQIMH 80

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Db 9 RTDEYQLFEELGKGAFSVVRRCMKIPTQGYAAKLIINTKKLSAR-DHOKLEREARIC-R 66
QY 81 LSEHPNVNRIKGTYESVFIHVMCEGGEFLDRIVSKGHFSEAEVAVKLIITILGVBEA 140
Db 67 LLKHPNIVRLHDSISEGPHYVDFDLVGTGELFEDIVAREYVSEADASHCIQIILSVNH 126
QY 141 CHSLGVNHRDLKPNFLFSPKDDAKLKTATDFGLSVFYKPGQYL-YDVVGSPPYVAPEVL 199
Db 127 CHLNGIVHRLDLKPNILLASKSGAAVLADEGLALEVQDQOQAFAGTAGTGYLSPEVL 186
QY 200 KK-CYGPEDVWSAGVILYLLSGVPPFWAETESGIFRQILQGLDFKSDPWTIIEAAK 258
Db 187 KDPYKGVDMWACGVILYLLSGVPPFWAETESGIFRQILQGLDFKSDPWTIIEAAK 246
QY 259 DLIYKMLSPKRRISAEALCHPWTVDQEAAPKPLDPAVLISRLKQFSOMNKKMALR 318
Db 247 DLINKMLTINPAKRITASEALKHPWCQRTSVASMMHRQETVDCLEKFNARRKLKG---A 303
QY 319 VTAERLSEIEGLKELFKMID-----TNSG-TITFEELKA---GLKRVGSELMESEIK 369
Db 304 ILTMTLATRNFAAKLLKPKDGVKSTESSNTTIEDVDKARKQBIKVTQOLIEA--- 360
QY 370 SLMDAADIDNSGTYDYGELAA 392
Db 361 -----INNGDFEAYT 370

RESULT 10
KCCL_RAT
ID KCCL_RAT STANDARD; PRT; 374 AA.
AC Q63450; Q63084;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Calcium/calmodulin-dependent protein kinase type I (EC 2.7.1.123)
DE (CAM kinase I).
GN CAMK1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
RP SEQUENCE FROM N.A. (37 KDA ISOFORM).
RX MEDLINE=94075341; PubMed=8253780;
RA Picciotto M.R., Czernik A.J., Nairn A.C.;
RT "Calcium/calmodulin-dependent protein kinase I. cDNA cloning and
RT identification of autophosphorylation site.";
RL J. Biol. Chem. 268:26512-26521(1993).
RN [2]
RP SEQUENCE FROM N.A. (42 KDA ISOFORM).
RC STRAIN-Sprague-Dawley; TISSUE=Lung;
RX MEDLINE=95035115; PubMed=7948038;
RA Cho F.S., Phillips K.S., Bogucki B., Weaver T.E.;
RT "Characterization of a rat cDNA clone encoding calcium/calmodulin-
RT dependent protein kinase I.";
RL Biochim. Biophys. Acta 1224:156-160(1994).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF SHORT FORM.
RC TISSUE=Brain;
RX MEDLINE=96182648; PubMed=8601311;
RA Goldberg J., Nairn A.C., Kuriyan J.;
RT "Structural basis for the autoinhibition of
RT calcium/calmodulin-dependent protein kinase I.";
RL Cell 84:875-887(1996).
CC -!- FUNCTION: PHOSPHORYLATES SYNAPSTIN I.
CC -!- CATALYTIC ACTIVITY: ATP + protein = ADP + O-Phosphoprotein.
CC -!- ENZYME REGULATION: ACTIVATED BY CA++/CALMODULIN. MUST BE
CC PHOSPHORYLATED TO BE MAXIMALLY ACTIVE.
CC -!- SUBUNIT: MONOMER.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CAMK SUBFAMILY.

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CC or send an email to license@isb-sib.ch)
CC -----
DR EMBL; L24907; AAA19670.1; -
DR EMBL; L26288; AAA66944.1; -
DR PDB; 1A06; 08-APR-98.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR Transferase; Serine/threonine-protein kinase; Calmodulin-binding;
KW Phosphorylation; ATP-binding; Alternative splicing; 3D-structure.
FT DOMAIN 20 276
FT PROTEIN KINASE.
FT NP_BIND 26 34
FT BINDING 49 49
FT ACT_SITE 141 141
FT MOD_RES 177 177
FT VARSPPLIC 323 374
FT TSEQGGQTASHGELTPTTAGGPAAGCCGCCDCVCFSGSELP
FT PAPPPSSRAMD -> HQPGGTGTD (IN 37 KDA
FT ISOFORM).
FT CONFLICT 112 112 F -> G (IN REF. 1).
FT CONFLICT 118 118 A -> R (IN REF. 1).
FT CONFLICT 309 309 A -> R (IN REF. 1).
FT SEQUENCE 374 AA; 41638 MW; 37889B3DEF033AB2 CRC64;
SQ
Query Match 22.7%; Score 589.5; DB 1; Length 374;
Best Local Similarity 41.6%; Pred. No. 4.7e-23;
Matches 124; Conservative 56; Mismatches 113; Indels 5; Gaps 4;
QY 18 QTPRLRDHYLLGKLGQGGTGYTLTEKSTSNANYACKSIPKRLKVCREDYDWEIQL 77
Db 12 QAEDIRDIYDFRDVLTGAFSEVLAEDKFTQKLVAKIAKKALEGKEG--SMENEIAV 69
QY 78 MHLSEHPNVNRIKGTYESVFIHVMCEGGEFLDRIVSKGHFSEAEVAVKLIITILGV 137
Db 70 LHKI-KHPNIVALLDDIYESGHHYLLIMQVSGGELFDRIVEKGFYTERDASRLIFQVLA 128
QY 138 VEACHSLGVNHRDLKPNFLFSPKDDAKLKTATDFGLSVFYKPGQYLVDVVGSPYVAPE 197
Db 129 VKYLHDLGIVHRLKPNLLYLLSGVPPFWAETESGIFRQILQGLDFKSDPWTIIEAAK 188
QY 198 VL-KKCYGPEDVWSAGVILYLLSGVPPFWAETESGIFRQILQGLDFKSDPWTIIEAAK 256
Db 189 VLAQPKYSKAVDCMSIGVIAIILCGYPFYDENDAKLFEQILKAEYEFDSPTWDDISDS 248
QY 257 AKDLIYKMLSPKRRISAEALCHPWTVDQEAAPKPLDPAVLISRLKQFSOMNKKIK 314
Db 249 AKDFIRHLMKDEPKRTCEQALQHPWIAQDTAL-DKNIHQSVSEQIKKFNASKWKQ 305
RESULT 11
KCCL_HUMAN
ID KCCL_HUMAN STANDARD; PRT; 370 AA.
AC Q14012;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Calcium/calmodulin-dependent protein kinase type I (EC 2.7.1.123)
DE (CAM kinase I).
GN CAMK1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95369239; PubMed=7641687;
RA Haribabu B., Hook S.S., Seibert M.A., Goldstein E.G., Tomhave E.D.,
RA Edelman A.M., Snyderman R., Means A.R.;
RT "Human calcium-calmodulin dependent protein kinase I: cDNA cloning,
RT domain structure and activation by phosphorylation at threonine-177
RT by calcium-calmodulin dependent protein kinase I kinase.";
RL EMBL J. 14:3679-3686(1995).
CC -!- FUNCTION: PHOSPHORYLATES SYNAPSIN I.
CC -!- CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.
CC -!- ENZYME REGULATION: ACTIVATED BY CA++/CALMODULIN. MUST BE
CC PHOSPHORYLATED TO BE MAXIMALLY ACTIVE.
CC -!- SUBUNIT: MONOMER.
CC -!- TISSUE SPECIFICITY: UBIQUITOUS.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CAMK SUBFAMILY.
CC -----
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CC -----
DR EMBL; L41816; AAA99458.1; -.
DR HSSP; Q63450; 1A06.
DR Genew; HGNC:1459; CAMK1.
DR MIM; 604998; -.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR Transferase; Serine/threonine-protein kinase; Calmodulin-binding;
KW Phosphorylation; ATP-binding; Alternative splicing.
FT DOMAIN 20 276 PROTEIN KINASE.
FT DOMAIN 287 321 CALMODULIN-BINDING (BY SIMILARITY).
FT NP_BIND 26 34 ATP (BY SIMILARITY).
FT BINDING 49 49 ATP.
FT ACT_SITE 141 141 BY SIMILARITY.
FT MOD_RES 177 177 PHOSPHORYLATION (AUTO-).
FT MUTAGEN 49 49 K->A: LOSS OF ACTIVITY.
SQ SEQUENCE 370 AA; 41337 MW; 57FA20CEG0FA76C CRC64;
Query Match 22.7%; Score 587.5; DB 1; Length 370;
Best Local Similarity 41.6%; Pred. No. 5.9e-23;
Matches 124; Conservative 55; Mismatches 114; Indels 5; Gaps 4;
QY 18 QTPRLRDHYLLGKLGQGFQFTYLTCTKSTSANVACKSIPKRLVCRDYEDVWREIQI 77
DB 12 QAEIRDYDFDVUGTGAFSVILAEKRTQKUNIAKIAKEALEGEG--SMENEIATV 69
QY 78 MHLHSEHPNVRIKGYEDSVFHVIMEYCEGGEFLDRIVSKGHFSREAVKLITILGV 137
DB 70 LHKI-KHPNIVALDDIYSGGHLXLMQLVSGGELDFRIVEKGFYTERDASRLIFQVLDA 128
QY 138 VTACHSLGVNHRDLAPENFLFSPKDDAKLKATDFGLSVFYKPGQVLYDVGSPPYVAPE 197
DB 129 VKYLDLGLVHVRDLKPNLLYXSLDEDSKIMLSDFGLSKMEDPGSVLSTACGTPGYVAPE 188
QY 198 VL-KKCYGPEIDVWAGVLYLILSGVPFFWAEETSGIFRILQCKLDFKSDPWPITSEA 256
DB 189 VLAQPKYSKAVCWSIGVTAYILLCGYPPFYDENAKLFEQILKAEYFDPSPYWDIDIS 248
QY 257 AKDLIVKMLERSPKKRISAEALCHFPWIVDEQAAPKPLDPAVLGRLKQFSOMNKIKK 314
DB 249 AKDFIHLMEKDPKRFCEQALQHPWTAGDTAL-DKNHQSVSGQIKKNFAKSKWKQ 305

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RESULT 12
KCC4_HUMAN
ID KC4_HUMAN STANDARD; PRT; 473 AA.
AC Q16566;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Calcium/calmodulin-dependent protein kinase type IV catalytic chain
DE (EC 2.7.1.123) (CAM kinase-GR) (CaMK IV).
GN CAMK4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94375404; PubMed=8089075;
RA Kitani T., Okuno S., Fujisawa H.;
RT "cDNA cloning and expression of human calmodulin-dependent protein
RT kinase IV.";
RL J. Biochem. 115:637-640(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Cerebellum, and Thymus;
RX MEDLINE=94252566; PubMed=8194751;
RA Bland M.M., Monroe R.S., Ohmstede C.A.;
RT "The cDNA sequence and characterization of the
RT Ca2+/calmodulin-dependent protein kinase-Gr from human brain and
RT thymus.";
RL Gene 142:191-197(1994).
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE=Blood;
RX MEDLINE=94149862; PubMed=8107230;
RA Mosialos G., Hanissian S.H., Jawahar S., Vara L., Kieff E.,
RA Chatila T.A.;
RT "A Ca2+/calmodulin-dependent protein kinase, Cam kinase-Gr, expressed
RT after transformation of primary human B lymphocytes by Epstein-Barr
RT virus (EBV) is induced by the EBV oncogene LMP1.";
RL J. Virol. 68:1697-1705(1994).
RN [4]
RP SEQUENCE FROM N.A.
RX TISSUE=Brain;
RA Strausberg R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: CALSPERMIN IS A HEAT-STABLE, ACIDIC, CALMODULIN-BINDING
CC PROTEIN.
CC -!- CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.
CC -!- SUBCELLULAR LOCATION: SUBSTANTIAL LOCALIZATION IN CERTAIN NEURONAL
CC NUCLEI (BY SIMILARITY).
CC -!- ALTERNATIVE PRODUCTS: CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE
CC TYPE IV CATALYTIC CHAIN AND CALSPERMIN ARE OBTAINED BY ALTERNATIVE
CC SPLICING.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CAMK SUBFAMILY.
CC -----
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CC -----
DR EMBL; D30742; BAA06403.1; -.
DR EMBL; L17000; AAA35639.1; -.
DR EMBL; L24959; AAA18251.1; -.
DR EMBL; BC016695; AAH16695.1; -.
DR HSSP; Q63450; 1A06.
DR Genew; HGNC:1464; CAMK4.
DR MIM; 114080; -.

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DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD000001; Euk_pkinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR Transferrase: Serine/threonine-protein kinase; ATP-binding;
KW Calmodulin-binding.
FT DOMAIN 46 300 PROTEIN_KINASE.
FT NP_BIND 52 60 ATP (BY SIMILARITY).
FT BINDING 75 75 ATP (BY SIMILARITY).
FT ACT_SITE 164 164 BY SIMILARITY.
FT DOMAIN 322 341 CALMODULIN-BINDING (POTENTIAL).
SQ SEQUENCE 473 AA; 51925 MW; EFEE5ES612326DC CRC64;

Query Match 22.3%; Score 578.5; DB 1; Length 473;
Best Local Similarity 37.2%; Pred. No. 2.1e-22;
Matches 140; Conservative 65; Mismatches 144; Indels 27; Gaps 10;

QY 22 LRHYLGKKLGGQGFYTYCTEKTSTANYACKSIPKRLVCREDEDVWREIQIMHHL 81
DB 42 LSDFEVESELGRGATSIYVRCKQGTQKPYALKVLAK-----TVDKKIVRTEIGVLLRL 96
QY 82 SEHPNVVRKIGTYEDSVFVHTVMEVCEGGLFDRIIVSKGHSEAEVAKLTKLTILGVVEAC 141
DB 97 S-HENIARKLEIFPTPEISLVLSVLTGGELFDRIIVKGYISEKDAVAKQIILEAVYL 155
QY 142 HSLGVMRHDLKPNFLDFSPKDDAKLAKATDFGLSVFVKPGQYLDVVGSPYVVAPEVLKK 201
DB 156 HENGIVHRDLKPNLLYATPAPDAPLAKIADGLSKIVHEQVLMKTVCGTGYCAPEILRG 215
QY 202 C-YGPEIDVWSAGVILLISGVPPFWAET--ESGIFRQIQLOGKLDKPSDPWPTTISRAKD 259
DB 216 CAYGPEVDMWSVGIITVILGCGFFPYDERGDQFMFRILNCEYFIFFSPWDEVSNAKD 275
QY 260 LIYKMLERSPKRISAEALCHPWIVDEQAAPDKLPDPAVLRSKLQFSOMNKKIKMALRV 319
DB 276 LVRLKLVDPKRLTFTQALQHPWTVG-KAANFVHMDTA-QKQLQEFNARKLKAAYKAV 333
QY 320 IA-BRL--SEEEIGLKEFLFKH-----IDFDSGTITFEF-----LKAGLKRGVSE 362
DB 334 VASRLGSSASSHSGSIQESHKASRDSP[IQDGNEDMKAIPGEKIQDGAQAAYKGAQAE 393
QY 363 LMESEIKSLMDAADI 378
DB 394 LMKVQALEKVKGADIN 409

RESULT 13
KCCD_RAT STANDARD; PRT; 533 AA.
AC P15791;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Calcium/calmodulin-dependent protein kinase type II delta chain (EC
DE 2.7.1.123) (Cam-kinase II delta chain) (Cam kinase II delta subunit)
DE (CaMK-II delta subunit).
GN CAMK2D.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90036861; PubMed=2553697;
RA Tobimatsu T., Fujisawa H.;
RT "Tissue-specific expression of four types of rat calmodulin-dependent
RT protein kinase II mRNAs.";
RL J. Biol. Chem. 264:17907-17912(1989).
RN [2]

SEQUENCE OF 314-533 FROM N.A.
RP STRAIN-Sprague-Dawley; TISSUE-Aorta, and Skeletal muscle;
RX MEDLINE=93300844; PubMed=8390994;
RA Schworer C.M., Rothblum L.I., Thekkumkara T.J., Singer H.A.;
RT "Identification of novel isoforms of the delta subunit of
RT Ca2+/calmodulin-dependent protein kinase II. Differential expression
RT in rat brain and aorta.";
RL J. Biol. Chem. 268:14443-14449(1993).
CC -1- FUNCTION: THIS KINASE MAY PLAY A ROLE IN NEUROTRANSMISSION.
CC -1- CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.
CC -1- ENZYME REGULATION: AUTOPHOSPHORYLATION OF CAM-KINASE II PLAYS AN
CC IMPORTANT ROLE IN THE REGULATION OF THE KINASE ACTIVITY.
CC -1- SUBUNIT: COMPOSED OF FOUR DIFFERENT CHAINS: ALPHA, BETA, GAMMA,
CC AND DELTA.
CC -1- ALTERNATIVE PRODUCTS: 4 ISOFORMS; DELTA 1 (SHOWN HERE), DELTA 2,
CC DELTA 3 AND DELTA 4; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: DELTA 1 IS THE PREDOMINANT FORM IN THE
CC BRAIN, DELTA 2 AND 3 PREDOMINATE IN THE AORTA AND DELTA 4
CC IN SKELETAL MUSCLE.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CAMK SUBFAMILY.

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EMBL: J05072; AAA40866.1; -
EMBL: L13406; AAA41479.1; -
EMBL: L13407; AAA41480.1; -
EMBL: L13408; AAA41481.1; -
EMBL: A34366; A34366.
PIR: A34366; A34366.
HSP: Q63450; IA06.
InterPro: IPR000719; Euk_pkinase.
InterPro: IPR002290; Ser_thr_pkinase.
Pfam: PF00069; pkinase; 1.
ProDom: PD000001; Euk_pkinase; 1.
SMART: SM00220; S_TKC; 1.
PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
Transferrase: Serine/threonine-protein kinase; Calmodulin-binding;
KW Phosphorylation; ATP-binding; Neurone; Alternative splicing.
FT DOMAIN 14 272 PROTEIN_KINASE.
FT NP_BIND 20 28 ATP (BY SIMILARITY).
FT BINDING 43 43 ATP (BY SIMILARITY).
FT ACT_SITE 136 136 BY SIMILARITY.
FT DOMAIN 291 301 CALMODULIN-BINDING (BY SIMILARITY).
FT VARSPLIC 329 362 MISSING (IN ISOFORM DELTA 2).
FT VARSPLIC 329 335 INKANV -> KRKSSV (IN ISOFORM DELTA 3).
FT VARSPLIC 337 359 MISSING (IN ISOFORM DELTA 3).
FT VARSPLIC 360 362 GNK -> QMM (IN ISOFORM DELTA 3).
FT VARSPLIC 349 362 MISSING (IN ISOFORM DELTA 4).
SQ SEQUENCE 533 AA; 60080 MW; E41BCB2B5A00E7CA CRC64;

Query Match 22.2%; Score 574.5; DB 1; Length 533;
Best Local Similarity 39.4%; Pred. No. 3.8e-22;
Matches 127; Conservative 54; Mismatches 134; Indels 7; Gaps 5;

QY 21 RLRDHYLGKKLGGQGFYTYCTEKTSTANYACKSIPKRLVCREDEDVWREIQIMHH 80
DB 9 RFTDEYQLFEELGKGAFSVVRCKMKTPTGOEYAKKIINTKKLSAR-DHOKLEAREIC-R 66
QY 81 LSEHPNVVRKIGTYEDSVFVHTVMEVCEGGLFDRIIVSKGHSEAEVAKLTKLTILGVVEA 140
DB 67 LLKHPNIVRLHDSISEEGFHYLVFDLTGTGGLFEDIVAREYSEADASHGCIQILESVNH 126
QY 141 CHSGVGMVRHDLKPNFLDFSPKDDAKLAKATDFGLSVFVKPGQYL-YDVVSGSPYVVAPEVL 199
DB 127 CHLNGIVHRDLKPNLLYATPAPDAPLAKIADGLSKIVHEQVLMKTVCGTGYCAPEIL 186

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RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND PARTIAL SEQUENCE.
RX MEDLINE=9128548; PubMed=1648230;
RA Ohmsted C.-A., Bland M.M., Merrill B.M., Sahyoun N.;
RT "Relationship of genes encoding Ca2+/calmodulin-dependent protein
RL kinase Gr and caldespermin: a gene within a gene";
RN proc. Natl. Acad. Sci. U.S.A. 88:5784-5788(1991).
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RX MEDLINE=91304387; PubMed=1649385;
RA Means A.R., Cruzalegui F., Lemaquerresse B., Needleman D.S.,
RA Slaughter G.R., Ono T.;
RT "A novel Ca2+/calmodulin-dependent protein kinase and a male germ
RT cell-specific calmodulin-binding protein are derived from the same
RT gene.";
RL Mol. Cell. Biol. 11:3960-3971(1991).
RN [3]
RP SEQUENCE OF 250-474 FROM N.A. (ISOFORM 1).
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=89174647; PubMed=2538431;
RA Ohmsted C.-A., Jenson K.F., Sahyoun N.;
RT "Ca2+/calmodulin-dependent protein kinase enriched in cerebellar
RT granule cells. Identification of a novel neuronal
RT calmodulin-dependent protein kinase.";
RL J. Biol. Chem. 264:5866-5875(1989).
RN [4]
RP SEQUENCE OF 306-474 FROM N.A. (ISOFORM 2), AND SEQUENCE OF 335-361.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=89123272; PubMed=2914893;
RA Ono T., Slaughter G.R., Cook R.G., Means A.R.;
RT "Molecular cloning sequence and distribution of rat caldespermin, a
RT high affinity calmodulin-binding protein.";
RL J. Biol. Chem. 264:2081-2087(1989).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RX MEDLINE=96094352; PubMed=7493991;
RA Sun Z., Means R.L., Lemaquerresse B., Means A.R.;
RT "Organization and analysis of the complete rat calmodulin-dependent
RT protein kinase IV gene.";
RL J. Biol. Chem. 270:29507-29514(1995).
CC -!- FUNCTION: CAM KINASE GR IS A NEURONAL-SPECIFIC PROTEIN KINASE,
CC ENRICHED IN CEREELLAR GRANULE CELLS.
CC -!- FUNCTION: CALDESPERMIN IS A HEAT-STABLE, ACIDIC, CALMODULIN-BINDING
CC PROTEIN.
CC -!- CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.
CC -!- ALTERNATIVE PRODUCTS: 2 isoforms; 1/calcium-calmodulin-dependent
CC protein kinase type IV catalytic chain (shown here) and
CC 2/caldespermin; are produced by alternative splicing.
CC -!- TISSUE SPECIFICITY: Isoform 1 is expressed in brain and isoform 2
CC is testis-specific.
CC -!- PTM: THE N-TERMINAL OF CALDESPERMIN IS BLOCKED.
CC -!- MISCELLANEOUS: The presence of an alternative promoter gives rise
CC to the testis-specific isoform 2/caldespermin protein.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CAMK SUBFAMILY.
CC
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CC
CC EMBL; M63334; AAA0865.1; -
CC DR EMBL; M74488; AAA0845.1; ALT_SEQ.
CC DR EMBL; M64757; AAA0856.1; -
CC DR EMBL; M64757; AAA0857.1; -
CC DR EMBL; J04600; AAA1867.1; -
CC DR EMBL; J04446; AAA0990.1; -
CC DR PIR; A41103; TVRTC4.
CC HSSP; O63450; 1A06.
CC InterPro; IPR000719; Euk_pkinase.
CC InterPro; IPR002290; Ser_thr_pkinase.

DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00106; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Calmodulin-binding; Testis; Alternative splicing.
FT DOMAIN 42 296 PROTEIN KINASE.
FT NP_BIND 48 56 ATP (BY SIMILARITY).
FT BINDING 71 71 BY SIMILARITY.
FT ACT_SITE 160 160 CALMODULIN-BINDING (POTENTIAL).
FT DOMAIN 318 337 POLY-GLU.
FT DOMAIN 393 399 POLY-GLU.
FT DOMAIN 403 413 MISSING (IN ISOFORM 2).
FT VARSPLIC 1 305 I -> M (IN REF. 2 AND 4).
FT CONFLICT 372 372 56F7AC5644DED23 CRC64;
SQ SEQUENCE 474 AA; 53133 MW; 56F7AC5644DED23 CRC64;
Query Match 22.1%; Score 572; DB 1; Length 474;
Best Local Similarity 34.1%; Pred. No. 4.5e-22;
Matches 142; Conservative 75; Mismatches 158; Indels 42; Gaps 11;
QY 3 TKPN-PRRPSNTVLPYQTPRLRDHYLLGKK-----LQGGQFGTYLCTEKST 48
DB 5 TVPSCPSPSCSSVTSSTENLVPDVIWDGSKRDPLSDFFVESELGSGATSIYRCKQKGT 64
QY 49 SANYACKSIPKRLKVCREDYEDVWREIQIMHHLSEHPNVVRIKTYEDSVFVHIVEYCE 108
DB 65 OKPYALKVLKK-----TVDKKIVRTIEIGVLLRLS-HPNIIKKEIFETPTETISIVLELV 118
QY 109 GGELFDRIYVSKGHSEERAVKLITKILGVVEACHSLGVWHRDLKPEFLFDPSPKDDAKLK 168
DB 119 GGELFDRIYVSKGHSEERAVKLITKILGVVEACHSLGVWHRDLKPEFLFDPSPKDDAKLK 178
QY 169 ATDFGLSVFYKPGQYLYDVGVSPYYVAPEVLKCC-YGPEIDVWVSAGVILYILLGVPPFW 227
DB 179 IADFGLSKIVEHQVLMKTVCGTGYCAPELLRGCAYGFEVDMWSVGIIITYILCGFEFFY 238
QY 228 AET-ESGIFRQILQGLDFKDPDPWTISEAAKDLIYKMLERSPKKRISAHEALCHPWIVD 286
DB 239 DERGDQFMFRILNCEYFYFISFWNDEVSLNAKDLVKKLIVLDPKKRLTTFQALQHPWVTG 298
QY 287 EQAAPDKPLDPAVLKRLKQFSQNMKIKKWLRVIAERLSEEEIGGLKELFKMIDTDSGT 346
DB 299 -KAANFVIMDTA-QKKLQEFFNARRKLKAAVAVVA---SSPLGSASSSHNIOESNKAS 352
QY 347 TTFEELKAGLKRKVGSELMESEIKSLMDAADIDNSGTIDYGFFLAATLHMKNMEREI 403
DB 353 SEAPQAQDGKDK--TDPLENKIQA-----GDHEAAKAAADETMKLQSEEV 395
Search completed: March 26, 2003, 13:10:50
Job time : 25 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 26, 2003, 12:08:22 ; Search time 75 Seconds
(without alignments)
1359.911 Million cell updates/sec

Title: US-09-848-806-1

Perfect score: 2593

Sequence: 1 METKPNRRPSNTVLPYQTP.....KNLNFNIADAFVGDEKSD 495

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21.*

- 1: sp-archaea.*
- 2: sp-bacteria.*
- 3: sp-fungi.*
- 4: sp-human.*
- 5: sp-invertebrate.*
- 6: sp-mammal.*
- 7: sp-mhc.*
- 8: sp-organelle.*
- 9: sp-phage.*
- 10: sp-plant.*
- 11: sp-rodent.*
- 12: sp-virus.*
- 13: sp-vertebrate.*
- 14: sp-unclassified.*
- 15: sp-rvivirus.*
- 16: sp-bacteria.*
- 17: sp-archaea.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2593	100.0	495	10 Q39016	Q39016 arabidopsis
2	2577	99.4	495	10 Q949P0	Q949P0 arabidopsis
3	2536	97.8	557	10 Q91QH7	Q91QH7 arabidopsis
4	2458	94.8	501	10 Q38869	Q38869 arabidopsis
5	2030	78.3	490	10 Q24430	Q24430 glycine max
6	1969.5	76.0	496	10 Q93X19	Q93X19 solanum tub
7	1844.5	71.1	490	10 Q42396	Q42396 arabidopsis
8	1773	68.4	551	10 Q9FXQ3	Q9FXQ3 oryza sativ
9	1752	67.6	492	10 Q04417	Q04417 zea mays (m
10	1751	67.5	487	10 Q43676	Q43676 phaseolus a
11	1745	67.3	554	10 Q04123	Q04123 zea mays (m
12	1742	67.2	556	10 Q38871	Q38871 arabidopsis
13	1739.5	67.1	578	10 Q93XJ0	Q93XJ0 solanum tub
14	1733.5	66.9	578	10 Q93VF3	Q93VF3 nicotiana t
15	1731	66.8	544	10 Q38872	Q38872 arabidopsis
16	1728	66.6	581	10 Q93YF4	Q93YF4 nicotiana t

17	1719	66.3	646	10 Q38870	Q38870 arabidopsis
18	1717.5	66.2	578	10 Q24460	Q24460 tortula rur
19	1709.5	65.9	573	10 P38838	P38838 cucurbita p
20	1709	65.9	483	10 Q39014	Q39014 arabidopsis
21	1708	65.9	581	10 Q93YF7	Q93YF7 nicotiana b
22	1700.5	65.6	484	10 Q9S2M3	Q9S2M3 arabidopsis
23	1672.5	64.5	639	10 Q82107	Q82107 zea mays (m
24	1640.5	63.3	583	10 Q9ZV15	Q9ZV15 arabidopsis
25	1630	62.9	451	10 Q41789	Q41789 zea mays (m
26	1592	61.4	542	10 Q9SNK9	Q9SNK9 oryza sativ
27	1587	61.2	542	10 Q65003	Q65003 oryza sativ
28	1531.5	59.1	548	10 Q9S7Z4	Q9S7Z4 marchantia
29	1524.5	58.8	548	10 Q8S786	Q8S786 marchantia
30	1509.5	58.2	528	10 Q8VYE7	Q8VYE7 arabidopsis
31	1506.5	58.1	528	10 Q9FMP5	Q9FMP5 arabidopsis
32	1484.5	57.3	540	10 Q81390	Q81390 nicotiana t
33	1482	57.2	531	10 Q949U0	Q949U0 arabidopsis
34	1482	57.2	531	10 Q9ZSA2	Q9ZSA2 arabidopsis
35	1480	57.1	518	10 Q9AXA7	Q9AXA7 oryza sativ
36	1480	57.1	531	10 Q41790	Q41790 zea mays (m
37	1475	56.9	347	10 Q941Q5	Q941Q5 psophocarpu
38	1473	56.8	553	10 Q8RW36	Q8RW36 lycopersico
39	1471.5	56.7	521	10 Q94KH6	Q94KH6 lycopersico
40	1469.5	56.7	542	10 Q9AR92	Q9AR92 medicago sa
41	1464.5	56.5	514	10 Q9ARI5	Q9ARI5 cucumis sat
42	1463.5	56.4	521	10 Q9C6P3	Q9C6P3 arabidopsis
43	1462	56.4	529	10 Q42479	Q42479 arabidopsis
44	1462	56.4	534	10 Q9FRK2	Q9FRK2 oryza sativ
45	1458.5	56.2	538	10 Q24431	Q24431 glycine max

ALIGNMENTS

RESULT 1

Q39016	PRELIMINARY;	PRT;	495 AA.
ID	Q39016		
AC	Q39016;		
DT	01-NOV-1996 (TrEMBLrel. 01, Created)		
DT	01-NOV-1996 (TrEMBLrel. 01, Last sequence update)		
DT	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)		
DE	Calcium-dependent protein kinase.		
GN	ACDPK2.		
OS	Arabidopsis thaliana (Mouse-ear cross).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;		
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsi.		
OX	NCBI_TaxID=3702;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=COLUMBIA;		
RX	MEDLINE=94959455; PubMed=8078458;		
RA	Urao T., Katagiri T., Mizoguchi T., Yamaguchi-Shinozaki K.,		
RA	Hayashida N., Shinozaki K.;		
RT	"Two genes that encode Ca2+-dependent protein kinases are induced by		
RT	drought and high-salt stresses in Arabidopsis thaliana.";		
RL	Mol. Gen. Genet. 244:331-340(1994).		
CC	-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.		
DR	EMBL; D21806; BAA04830.1; -		
DR	HSSP; P02593; 1FW4.		
DR	InterPro; IPR002048; EF-hand.		
DR	InterPro; IPR00719; Euk_pkinase.		
DR	InterPro; IPR002290; Ser_thr_pkinase.		
DR	Pfam; PF00036; ehand; 4.		
DR	Pfam; PF00069; pkinase; 1.		
DR	ProDom; PD000001; Euk_pkinase; 1.		
DR	ProDom; PD000012; EF-hand; 2.		
DR	SMART; SM00054; Ehf; 4.		
DR	SMART; SM00220; S_TKc; 1.		
DR	PROSITE; PS00018; EF_HAND; UNKNOWN_4.		
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.		
DR	PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.		
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.		

KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 495 AA; 55867 MW; 5909A45124C3A6D CRC64;

Query Match 100.0%; Score 2593; DB 10; Length 495;
Best Local Similarity 100.0%; Pred. No. 9.5e-183;
Matches 495; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 METKPNRPSTNVLPTQPRLDHYLLGKLGKGGGFGTTLCTEKSTANTACKSIPKR 60
DB 1 METKPNRPSTNVLPTQPRLDHYLLGKLGKGGGFGTTLCTEKSTANTACKSIPKR 60
QY 61 KLVCRDIEDVREIOMHHLSEHPNVRKGTIYEDSVFVHIVMEYCEGGELEFDRIVSKG 120
DB 61 KLVCRDIEDVREIOMHHLSEHPNVRKGTIYEDSVFVHIVMEYCEGGELEFDRIVSKG 120
QY 121 HFSEREAVKLITILGVVEACHSLGVNHRDLKPENFLFDSPKDDAKLKATDFGLSVFYKP 180
DB 121 HFSEREAVKLITILGVVEACHSLGVNHRDLKPENFLFDSPKDDAKLKATDFGLSVFYKP 180
QY 181 GOVLYDVVGSPPYVAPEVLKCKYCPEDVWSAGVILYLLSGVPPFWAETESGIFRQILQ 240
DB 181 GOVLYDVVGSPPYVAPEVLKCKYCPEDVWSAGVILYLLSGVPPFWAETESGIFRQILQ 240
QY 241 GKLDKSDPWTPTTISEAAKOLLYKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAYL 300
DB 241 GKLDKSDPWTPTTISEAAKOLLYKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAYL 300
QY 301 SRLKQFSQMNKIKKMLRVTAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLRVKG 360
DB 301 SRLKQFSQMNKIKKMLRVTAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLRVKG 360
QY 361 SELMESEIKSLMDAADIDNSGTIDYGEFLAATLHMNMKEREELVAAFSDFDKDGSYIT 420
DB 361 SELMESEIKSLMDAADIDNSGTIDYGEFLAATLHMNMKEREELVAAFSDFDKDGSYIT 420
QY 421 IDELQSACTEFGLCDTPLDDMIKEIDLNDGKIDFSEFTAMMRKGDGVGRSRTMMKNLNF 480
DB 421 IDELQSACTEFGLCDTPLDDMIKEIDLNDGKIDFSEFTAMMRKGDGVGRSRTMMKNLNF 480
QY 481 NIADAFGVGDKESDD 495
DB 481 NIADAFGVGDKESDD 495

RESULT 2
Q949P0 PRELIMINARY; PRT; 495 AA.

ID Q949P0
AC Q949P0
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Putative calcium-dependent protein kinase SK5.
GN F1504.8.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamada K., Liu S.X., Pham P.K., Banh J., Banno F., Dale J.M.,
RA Goldsmith A.D., Jiang P.X., Lee J.M., Onodera C.S., Quach H.L.,
RA Tang C., Toriumi M., Yamamura Y., Yu G., Yu S., Bowser L.,
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kaniya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E., Lam B.,
RA Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
RA Sakurai T., Satou M., Seki M., Shinn P., Southwick A.,
RA Shinzaki K., Davis R.W., Ecker J.R., Theologis A.,
RT "Full length cDNA of gene F1504.8 (GI:8778378)."
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY050981; AAK93658.1;
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000719; Euk_pkinase.

DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00036; ehand; 4.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 1.
DR ProDom; PD000012; EF-hand; 2.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_4.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.
KW ATP-binding; Kinase; Transferase.
SQ SEQUENCE 495 AA; 55916 MW; 2DD0ED8C234EF27 CRC64;

Query Match 99.4%; Score 2577; DB 10; Length 495;
Best Local Similarity 99.6%; Pred. No. 1.4e-181;
Matches 493; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 METKPNRPSTNVLPTQPRLDHYLLGKLGKGGGFGTTLCTEKSTANTACKSIPKR 60
DB 1 METKPNRPSTNVLPTQPRLDHYLLGKLGKGGGFGTTLCTEKSTANTACKSIPKR 60
QY 61 KLVCRDIEDVREIOMHHLSEHPNVRKGTIYEDSVFVHIVMEYCEGGELEFDRIVSKG 120
DB 61 KLVCRDIEDVREIOMHHLSEHPNVRKGTIYEDSVFVHIVMEYCEGGELEFDRIVSKG 120
QY 121 HFSEREAVKLITILGVVEACHSLGVNHRDLKPENFLFDSPKDDAKLKATDFGLSVFYKP 180
DB 121 HFSEREAVKLITILGVVEACHSLGVNHRDLKPENFLFDSPKDDAKLKATDFGLSVFYKP 180
QY 181 GOVLYDVVGSPPYVAPEVLKCKYCPEDVWSAGVILYLLSGVPPFWAETESGIFRQILQ 240
DB 181 GOVLYDVVGSPPYVAPEVLKCKYCPEDVWSAGVILYLLSGVPPFWAETESGIFRQILQ 240
QY 241 GKLDKSDPWTPTTISEAAKOLLYKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAYL 300
DB 241 GKLDKSDPWTPTTISEAAKOLLYKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAYL 300
QY 301 SRLKQFSQMNKIKKMLRVTAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLRVKG 360
DB 301 SRLKQFSQMNKIKKMLRVTAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLRVKG 360
QY 361 SELMESEIKSLMDAADIDNSGTIDYGEFLAATLHMNMKEREELVAAFSDFDKDGSYIT 420
DB 361 SELMESEIKSLMDAADIDNSGTIDYGEFLAATLHMNMKEREELVAAFSDFDKDGSYIT 420
QY 421 IDELQSACTEFGLCDTPLDDMIKEIDLNDGKIDFSEFTAMMRKGDGVGRSRTMMKNLNF 480
DB 421 IDELQSACTEFGLCDTPLDDMIKEIDLNDGKIDFSEFTAMMRKGDGVGRSRTMMKNLNF 480
QY 481 NIADAFGVGDKESDD 495
DB 481 NIADAFGVGDKESDD 495

RESULT 3
Q9LOH7 PRELIMINARY; PRT; 557 AA.

ID Q9LOH7
AC Q9LOH7
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE F1504.8.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Ecker J.R.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Ecker J.R.;

Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.

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SEQUENCE FROM N.A.

Chen R., Shin P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
Khan S., Kim C., Altai H., Bei B., Chin C., Chio J., Choi E.,
Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,
Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsy N.,
Ravayer M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
Thayer A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
Theologis A., Ecker J.;
Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.

-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

EMBL; AC007887; AAF79386.1; -;
HSP; P02593; 1FW4.
InterPro: IPR002048; EF-hand.
InterPro: IPR000719; Euk_pkinase.
InterPro: IPR002290; Ser_thr_pkinase.
Pfam: PF00036; ehand; 4.
Pfam: PF00069; pkinase; 1.
ProDom: PD000001; Euk_pkinase; 1.
ProDom: PD000012; EF-hand; 2.
SMART; SM00054; EFh; 4.
SMART; SM00220; S_TKc; 1.
PROSITE; PS00018; EF_HAND; UNKNOWN_4.
PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Serine/threonine-protein kinase; Transferase.

SEQUENCE 557 AA; 63397 MW; 79285A5A6B3A240B CRC64;

Query Match 97.8%; Score 2536; DB 10; Length 557;
Best Local Similarity 88.5%; Pred. No. 1.8e-178;
Matches 493; Conservative 0; Mismatches 17; Indels 62; Gaps 1;

1 1 METKNRPSNTVLPYQTPRLRDHYLLGKLGQGGQFGTYLCTEKSTSANVACKSIPKR 60
|||||
1 1 METKNRPSNTVLPYQTPRLRDHYLLGKLGQGGQFGTYLCTEKSTSANVACKSIPKR 60
QY 61 KLVCRDIEDVWREIQIMHLLSEHPNVVRIKGTYESDVVFHVMEVCEGGEFLDRIVSKG 120
|||||
Db 61 KLVCRDIEDVWREIQIMHLLSEHPNVVRIKGTYESDVVFHVMEVCEGGEFLDRIVSKG 120
QY 121 HFSREAVKLIKTILGVVEACHSLGVHMDLKPENFLDSPKDDAKLATDGLSVFYKRP 180
|||||
Db 121 HFSREAVKLIKTILGVVEACHSLGVHMDLKPENFLDSPKDDAKLATDGLSVFYKRP 180
QY 181 ----- 180
Db 181 GLIFLWLIDSLILQLFWLFFVSMNRKLIKQSGFLIETGLLCFIWIANRNKVFEGMYRFD 240
QY 181 --GQYLVDVWGSPYVAVELKCKYGPEDVWSAGVILYLLSGVPPFWAETESGIFRQI 238
|||||
Db 241 LFGQYLVDVWGSPYVAVELKCKYGPEDVWSAGVILYLLSGVPPFWAETESGIFRQI 300
QY 239 LOGKLDKSDPWTPTISEAAKLIYKMLERSPKKRISAHEALCPHWIVDEQAAPDKPLDPA 298
|||||
Db 301 LOGKLDKSDPWTPTISEAAKLIYKMLERSPKKRISAHEALCPHWIVDEQAAPDKPLDPA 360
QY 299 VLSRLKQFSQMNKIKKMLRVIAERLSEEEIGLKLPMIDTDSGTTTFPEELKAGLR 358
|||||
Db 361 VLSRLKQFSQMNKIKKMLRVIAERLSEEEIGLKLPMIDTDSGTTTFPEELKAGLR 420
QY 359 VGSSELMSEIKSLMDAADTDSGTTIDYGEFLAATLHMKNKWEREELIVAFSDFDKDGSY 418
|||||
Db 421 VGSSELMSEIKSLMDAADTDSGTTIDYGEFLAATLHMKNKWEREELIVAFSDFDKDGSY 480
QY 419 ITIDELQSACTEFLGLCDTPLDDMKIEIDLNDGKIDFSEFTAMRRKGDGVRSRMTMKNL 478
|||||
Db 481 ITIDELQSACTEFLGLCDTPLDDMKIEIDLNDGKIDFSEFTAMRRKGDGVRSRMTMKNL 540
QY 479 NFNIAFAFGVGEKSD 495
|||||
Db 541 NFNIAFAFGVGEKSD 557

RESULT 4

Q38869 PRELIMINARY; PRT; 501 AA.

DT 01-NOV-1996 (TREMELrel. 01, Created)

DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)

DT 01-JUN-2002 (TREMELrel. 21, Last annotation update)

DE Calmodulin-domain protein kinase CDPK isoform 4 (Fragment).

GN CPK4 OR T52P22.10 OR AT4G09570.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.

OC NCBI_TaxID=3702;

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLOMBIA;
RA McCombie W.R.;
RT "Arabidopsis thaliana Genomic Sequence, Chromosome IV.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.

RN [2]
RP SEQUENCE FROM N.A.
RA McCombie R.W., Spiegel L.A., Huang E.N., Nascimento L.U.,
de la Bastide M., Vil D.M., Preston R.R., Matero A., Shah R., O'Shaughnessy A., Rodriguez M.,
O'Shaughnessy A., Rodriguez M., Shekher M., Schutz K., See L.H.,
Swaby I., Habermann K., Dedhia N.N., Mewes H.W., Lemcke K.,
Mayer K.F.X.;
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RN [3]
RP SEQUENCE FROM N.A.
RA Spiegel L.A., Huang E.N., Nascimento L.U., de la Bastide M., Vil D.M.,
Preston R.R., Matero A., Shah R., O'Shaughnessy A., Rodriguez M.,
Shekher M., Schutz K., See L.H., Swaby I., Habermann K., Dedhia N.N.,
Mewes H.W., Lemcke K., Mayer K.F.X.;
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

DR EMBL; U31752; AA803243.1; -;
DR EMBL; AL161831; CAB82124.1; -;
DR EMBL; AL161515; CAB78080.1; -;
DR HSP; P02593; 1FW4.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam; PF00036; ehand; 4.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Euk_pkinase; 1.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 4.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_4.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Kinase; Serine/threonine-protein kinase.
FT NON_TER 1
SQ SEQUENCE 501 AA; 56416 MW; C709C17DEAF74B70 CRC64;

Query Match 94.8%; Score 2458; DB 10; Length 501;
Best Local Similarity 94.8%; Pred. No. 8.6e-173;
Matches 470; Conservative 9; Mismatches 13; Indels 4; Gaps 1;

QY 4 KPNRPSNTVLPYQTPRLRDHYLLGKLGQGGQFGTYLCTEKSTSANVACKSIPKRILV 63
|||||
Db 3 KPNRPSNTVLPYQTPRLRDHYLLGKLGQGGQFGTYLCTEKSTSANVACKSIPKRILV 62
QY 64 CREDYEDVWREIQIMHLLSEHPNVVRIKGTYESDVVFHVMEVCEGGEFLDRIVSKGHS 123
|||||
Db 63 CREDYEDVWREIQIMHLLSEHPNVVRIKGTYESDVVFHVMEVCEGGEFLDRIVSKGHS 122

Query Match 78.3%; Score 2030; DB 10; Length 490;
 Best Local Similarity 81.1%; Pred. No. 2.8e-141;
 Matches 386; Conservative 43; Mismatches 45; Indels 2; Gaps 2;

QY 14 VLVPQPRLDHYLGLKGGOGFGTTLCTEKSTANYACKSIPKRLKLYCREDYEDVWR 73
 DB 12 VLVPQARLDHYLGLKGGOGFGTTLCTHKVTKLYACKSIPKRLKLYCREDYEDVWR 71
 QY 74 EIQIMHLSHPPNVRIKGTEDSVFVHYVMEVCEGGELEFDRIVSKGHFSERAVKLIKT 133
 DB 72 EIQIMHLSHPPNVRIKGTEDSVFVHYVMEVCEGGELEFDRIVSKGHFSERAVKLIKT 131
 QY 134 ILGVVEACHSLGVNHRDLKPNFLDFSPKDDAKLKAEDFGLSVFKPGQYLYDVVGSPPY 193
 DB 132 ILGVVEACHSLGVNHRDLKPNFLDFSPKDDAKLKAEDFGLSVFKPGQYLYDVVGSPPY 191
 QY 194 VAPVLAACKYGPETDVMSAGVILYLLSGVPPFWAETESGIFRQILQKLFKSDPWPTI 253
 DB 192 VAPVLAACKYGPETDVMSAGVILYLLSGVPPFWAETESGIFRQILQKLFKSDPWPTI 251
 QY 254 SEAAKDIYKMLERSPKKRISAEHALCHPWIVDEQAAPDKPLDPVLSRLKQFSOMNKK 313
 DB 252 SENAKELVKQMLDRPKKRISAEHALCHPWIVDEQAAPDKPLDPVLSRLKQFSOMNKK 310
 QY 314 KMALRVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLKRVSSELSKSLMD 373
 DB 311 KMALRVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLKRVSSELSKSLMD 370
 QY 374 AADIDNSGTIDYGEFLAATLHNMKMEREEILVAAFSDFDKDGGVYITIDELOQACKDFSL 433
 DB 371 AADIDNSGTIDYGEFLAATLHNMKMEREEILVAAFSDFDKDGGVYITIDELOQACKDFSL 430
 QY 434 CDTPLDDMIKEIDLNDGKIDFSEFTAMMRKGD-GVGRSRTMKNLNENIADAFGV 488
 DB 431 GDVHDEMKEITDQNDGRIDYAEFAAMMKGDPNMGRSRTMKNLNENIADAFGV 486

RESULT 6
 Q93X19 PRELIMINARY; PRT; 496 AA.
 AC Q93X19; PRELIMINARY; PRT; 496 AA.
 DT 01-DEC-2001 (TremBLrel. 19, Created)
 DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TremBLrel. 20, Last annotation update)
 DE Calcium dependent protein kinase.
 GN R1C0PK2.
 OS Solanum tuberosum (Potato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4113;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lee J.-Y., Yoo B.-C., Harmon A.C.;
 RC Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
 RT -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 RT EMBL: U69173; AAB80692.1; -;
 DR HSP: P02588; 1PON.
 DR InterPro: IPR002048; EF-hand.
 DR InterPro: IPR000719; Euk.pkinase.
 DR InterPro: IPR002290; Ser_thr.pkinase.
 DR Pfam: PF00036; ehand; 4.
 DR ProDom: PD000001; Euk.pkinase; 1.
 DR ProDom: PD000012; EF-hand; 2.
 DR SMART: SM00054; EFh; 4.
 DR SMART: SM00220; S_TKc; 1.
 DR PROSITE: PS00018; EF_HAND; UNKNOWN_4.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
 DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 490 AA; 55164 MW; 233C411CAA43E0F CRC64;

QY 124 EREAVKLIKTILGVVEACHSLGVNHRDLKPNFLDFSPKDDAKLKAEDFGLSVFKPGQY 183
 DB 123 EREAAKLIKTILGVVEACHSLGVNHRDLKPNFLDFSPKDDAKLKAEDFGLSVFKPGQY 182
 QY 184 LYDVVGSPPYVAPVLAACKYGPETDVMSAGVILYLLSGVPPFWAETESGIFRQILQK 243
 DB 183 LYDVVGSPPYVAPVLAACKYGPETDVMSAGVILYLLSGVPPFWAETESGIFRQILQ 242
 QY 244 DFKSDPWPTIIEAAKDIYKMLERSPKKRISAEHALCHPWIVDEQAAPDKPLDPVLSRL 303
 DB 243 DFKSDPWPTIIEAAKDIYKMLERSPKKRISAEHALCHPWIVDEQAAPDKPLDPVLSRL 302
 QY 304 KQFSOMNKKIKMALRVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLKRVSSEL 363
 DB 303 KQFSOMNKKIKMALRVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLKRVSSEL 362
 QY 364 MESSEIKSLMDAADIDNSGTIDYGEFLAATLHNMKMEREEILVAAFSDFDKDGGVYITIDE 423
 DB 363 MESSEIKSLMDAADIDNSGTIDYGEFLAATLHNMKMEREEILVAAFSDFDKDGGVYITIDE 422
 QY 424 LQACTEGLCDTFLDDMIKEIDLNDGKIDFSEFTAMMRKGDGVGRSRTMKNLNENIA 483
 DB 423 LQACTEGLCDTFLDDMIKEIDLNDGKIDFSEFTAMMRKGDGVGRSRTMKNLNENIA 482
 QY 484 DAFGVGG-EEKSD 495
 DB 483 EAFGVEDTSSTAKSD 498

RESULT 5
 O24430 PRELIMINARY; PRT; 490 AA.
 ID O24430
 AC O24430;
 DT 01-JAN-1998 (TremBLrel. 05, Created)
 DT 01-JAN-1998 (TremBLrel. 05, Last sequence update)
 DT 01-MAR-2002 (TremBLrel. 20, Last annotation update)
 DE Calmodulin-like domain protein kinase isoenzyme beta.
 OS Glycine max (Soybean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC euroids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 OX NCBI_TaxID=3847;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA McKendree W.L., Doostdar H., McColium T.G., Mayer R.T.;
 RC "cDNA cloning and expression of a gene (Accession No. 297064) from
 RT Citrus paradisi roots similar to bacterial YN1 and HEAH10 proteins
 RT and an mRNA from Brassica oleracea that is wound and dark inducible
 RT (PGR97-127).";
 RL Plant Physiol. 115:314-314(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Lee J.-Y., Yoo B.-C., Harmon A.C.;
 RC Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
 RT -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC EMBL: U69173; AAB80692.1; -;
 DR HSP: P02588; 1PON.
 DR InterPro: IPR002048; EF-hand.
 DR InterPro: IPR000719; Euk.pkinase.
 DR InterPro: IPR002290; Ser_thr.pkinase.
 DR Pfam: PF00036; ehand; 4.
 DR ProDom: PD000001; Euk.pkinase; 1.
 DR ProDom: PD000012; EF-hand; 2.
 DR SMART: SM00054; EFh; 4.
 DR SMART: SM00220; S_TKc; 1.
 DR PROSITE: PS00018; EF_HAND; UNKNOWN_4.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
 DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 490 AA; 55164 MW; 233C411CAA43E0F CRC64;

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SQ SEQUENCE 496 AA; 55774 MW; EC41F7AED33B6DD5 CRC64;
Query Match 76.0%; Score 1969.5; DB 10; Length 496;
Best Local Similarity 76.6%; Pred. No. 8.3e-137;
Matches 377; Conservative 55; Mismatches 53; Indels 7; Gaps 4;

QY 1 METKP--NPRPSNTVLPYOTPRLRDHYLLGKLGQGFQGTLYLCTEKSANVACKSIP 58
DQ 1 MEKPATPEPKSSVWVLPYKQSLQSLYTGKLGQGFQGTTHLCLIEKSSGNLYACKTIP 60
QY 59 KRKLVCREDYEDVWREIQIMHLSHPNVVRIKGTYESVFEVHIVMEVCEGELFDRLVS 118
DQ 61 KKKLKICKEDYEDVWREIQIMHLSHPNVVRIKGTYESVFEVHIVMEVCEGELFDRLVS 120
QY 119 KGHSEAEVLIKILGVVEACHSLGVMHRLDLPENFLDPSKDDAKLKATDGLSVFY 178
DQ 121 KGHYSEREAALKILITVGVVEACHSLGVMHRLDLPENFLDPSKDDAKLKATDGLSVFY 180
QY 179 KPGQVLYDVVGSPIYVAVPEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETESGIFRQI 238
DQ 181 KPGFTSDVGSPIYVAVPEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETESGIFRQI 240
QY 239 LQGLDKFSDPWTISEAAKDLIYKMLSPKPKRISAEALCHPWIVDEQAAPKPLDPA 298
DQ 241 LRGKLDLSEPPGSDSADKILRLDRNPKRLTAHEVLCHPWIVDTVAPDKPLDSA 300
QY 299 VLSRLKQFSQNMKIKKMLRVIAERLSEEEIGGLKELFKMIDTNSGTTITFEELKAGLR 358
DQ 301 VLSRLKQFSQNMKIKKMLRVIAERLSEEEIGGLKELFKMIDTNSGTTITFEELKAGLR 360
QY 359 VGSSELMSEIKSLMDAADIDNSGTIDYGEFLAATLHMNMKMEREEILVAAFSDFKDGSY 418
DQ 361 VGSSELMSEIKSLMDAADIDNSGTIDYGEFLAATLHMNMKMEREEILVAAFSDFKDGSY 420
QY 419 ITIDELQACTEFGLCDPFLDDMIKEIDLNDGKIDFSEFTAMRKGDG--VGRSKTMMK 476
DQ 421 ITIDELQACTEFGLCDPFLDDMIKEIDLNDGKIDFSEFTAMRKGDG--VGRSKTMMK 478
QY 477 NLNFIADAFV 488
DQ 480 NL--NLGEALGL 489

RESULT 7
Q42396 PRELIMINARY; PRT; 490 AA.
AC Q42396;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Calcium-dependent protein kinase.
GN CDPK9.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Hong Y., Takano M., Liu C.M., Gasch A., Chye M.L., Tan C.T., Koh C.C.,
RA Chua N.H.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=20181125; PubMed=10718197;
RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence
RT features of the regions of 3,076,755 bp covered by sixty P1 and TAC
RT clones.";
RL DNA Res. 7:31-63(2000).
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-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC EMBL; U20626; AAA67657.1; -;
DR EMBL; U20388; AAA67653.1; -;
DR EMBL; AB025633; BAA97242.1; -;
DR HSP; P02588; IPON.
DR InterPro; IPR02048; EF-hand.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR022290; Ser_thr_kinase.
DR Pfam; PF00036; ehand; 4.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 1.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; Efh; 4.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_4.
DR PROSITE; PS0107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 490 AA; 55379 MW; 0315346396585264 CRC64;

Query Match 71.1%; Score 1844.5; DB 10; Length 490;
Best Local Similarity 73.1%; Pred. No. 1.3e-127;
Matches 353; Conservative 55; Mismatches 68; Indels 7; Gaps 2;

QY 1 METKPNRPSPNTVLPYOTPRLRDHYLLGKLGQGFQGTLYLCTEKSANVACKSIPKR 60
DQ 1 MANKPRTR---WVLPYKTKNVEDNYFLGVLGQGFQGTFLCTHKQTKGQKLACKSIKPR 56
QY 61 KLVCREDEYEDVWREIQIMHLSHPNVVRIKGTYESVFEVHIVMEVCEGELFDRLVSKG 120
DQ 63 KLVCREDEYEDVWREIQIMHLSHPNVVRIKGTYESVFEVHIVMEVCEGELFDRLVSKG 116
QY 57 KLLQGEDYDDVLRLEIQIMHLSHPNVVRIKGTYESVFEVHIVMEVCEGELFDRLVSKG 180
DQ 121 HFSEREAALKILITVGVVEACHSLGVMHRLDLPENFLDPSKDDAKLKATDGLSVFYK 176
DQ 117 HYSEREAALKILITVGVVEACHSLGVMHRLDLPENFLDPSKDDAKLKATDGLSVFYK 176
QY 181 GOYLYDVVGSPIYVAVPEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETESGIFRQILQ 240
DQ 177 GEAFSELVGSPIYVAVPEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETESGIFRQILQ 236
QY 241 GKLDKSDPWTISEAAKDLIYKMLSPKPKRISAEALCHPWIVDEQAAPKPLDPAVL 300
DQ 237 GKLEFEINPWPSTISEAAKDLIYKMLSPKPKRISAEALCHPWIVDEQAAPKPLDPAVL 296
QY 301 SRLKQFSQNMKIKKMLRVIAERLSEEEIGGLKELFKMIDTNSGTTITFEELKAGLRV 360
DQ 297 SRLKQFSQNMKIKKMLRVIAERLSEEEIGGLKELFKMIDTNSGTTITFEELKAGLRV 356
QY 361 SELMESEIKSLMDAADIDNSGTIDYGEFLAATLHMNMKMEREEILVAAFSDFKDGSYIT 420
DQ 357 SELMESEIKSLMDAADIDNSGTIDYGEFLAATLHMNMKMEREEILVAAFSDFKDGSYIT 416
QY 421 IDELOQACTEFGLCDPFLDDMIKEIDLNDGKIDFSEFTAMRKGDG---RMMKN 477
DQ 417 IDELOQACTEFGLCDPFLDDMIKEIDLNDGKIDFSEFTAMRKGDG---RMMKN 476
QY 478 LNF 480
DQ 477 LNF 479

RESULT 8
Q9FXQ3 PRELIMINARY; PRT; 551 AA.
ID Q9FXQ3;
AC Q9FXQ3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE OSCDPK7.
GN OSCDPK7.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RX MEDLINE=20387027; PubMed=10929125;
RA Saijo Y., Hata S., Kiyozuka J., Shimamoto K., Izui K.;
RT "Over-expression of a single Ca2+-dependent protein kinase confers
RT both cold and salt/drought tolerance on rice plants.";
RL Plant J. 23:319-327(2000).
DR EMBL; AB042550; BAB1688.1; -
DR HSSP; P02593; 1CTR.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00036; ehand; 4.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 1.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; Efh; 4.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_3.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00108; Serine/threonine-protein kinase; Transferase.
KW ATP-binding; Transferase.
SQ SEQUENCE 551 AA; 60966 MW; B479A089EF287A7B CRC64;

Query Match 68.4%; Score 1773; DB 10; Length 551;
Best Local Similarity 71.2%; Pred. No. 2.9e-122;
Matches 339; Conservative 53; Mismatches 82; Indels 2; Gaps 2;

QY 13 TVLPYQTPRLRDHYLLGKLGQGGFTYTLCTEKSTSANVACKSIKPKKLVCREDDYDVW 72
DB 75 SVLGHPPTNLRDLVAMGRKLGQGGFTYTLCTELSTGVYACKSISKRLITKEDVDV 134
QY 73 REIQIMHLSHPNVRIKGTYESVFVHYVMEVCEGELFDRIVSKGHSEREAVALIK 132
DB 135 REIQIMHLSGHKNVVAIKGAYEDQVYVHYVMELCAGSELFDRIIQGHYSEKAAALTR 194
QY 133 TILGVVACHSLGVHMRDLKPFENFLDSPKDDAKLKATDFGLSVFYKPGQYLDVVGSPY 192
DB 195 IIVGVVACHSLGVHMRDLKPFENFLANLKDLSLKALDFGLSVFYKPGQYLDVVGSPY 254
QY 193 YVAPEVLKCKYGPETDVMWSAGVILYLLSGVPPFWAETESGIFRQILQGLDKFSDPWT 252
DB 255 YVAPEVLKCKYGPETDVMWSAGVILYLLSGVPPFWAETESGIFRQILQGLDKFSDPWPV 314
QY 253 ISEAKDLIYKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAVLSRLKQFSQMNKI 312
DB 315 ISEAKDLIYKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAVLSRLKQFSQMNKI 374
QY 313 KKMALRVIAERLSEEEIGGLKELFKMIDTNSGTTIFELKAGLRKRVGSELMESEIKSLM 372
DB 375 KKMALRVIAERLSEEEIGGLKELFKMIDTNSGTTIFELKAGLRKRVGSELMESEIKSLM 434
QY 373 DAADTNSGTTIDYGFELAAATHMNMKEREELVAAFSDFDKDGSYIITDELQSACTEFG 432
DB 435 DAADTNSGTTIDYGFELAAATHMNMKEREELVAAFSDFDKDGSYIITDELQSACTEFG 494
QY 433 LCDTPLDMIKEDLDNCKIDFSEFTAMRRKGD-GVGRSTRTMKNLNFNLIADAFG 487
DB 495 MPDAFLDDVINEADQNDNDIGYGEFVAMTKGNMGVGR-RTMRNSLNLSMRDAPG 549

RESULT 9
O04417 PRELIMINARY; PRT; 492 AA.
ID O04417
AC O04417;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
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Db 374 DAADIDNSGTIDYIEFTAAFLHLNKLREHLLVAAPSYFDKDGSGYITVDELQACKEHN 433
QY 433 LCOTPLDDMIKEIDLDNDGKIDSEFTAMMRKGD-GVGRSRTMMKNLNFNIAD 484
Db 434 MPDAFLDDVINEADQNDGRIDYGEFVAMTKGMVGVR-RTMRNSLNLSMRD 485

RESULT 10
Q43676
ID Q43676 PRELIMINARY; PRT; 487 AA.
AC Q43676;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Calcium dependent protein kinase.
GN CDPK.
OS Phaseolus aureus (Mung bean) (Vigna radiata).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
OX NCBI_TaxID=3916;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=RWILCZ, AND CV. BERKEN; TISSUE=ETIOLATED HYPOCOTYL;
RX MEDLINE=96311003; PubMed=8704124;
RA Botella J.R., Arteca J.M., Somodevilla M., Arteca R.N.;
RT "Calcium-dependent protein kinase gene expression in response to
RT physical and chemical stimuli in mungbean (Vigna radiata).";
RL Plant Mol. Biol. 30:1129-1137(1996).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: U08140; AAC49405.1; -
DR HSSP: Q63450; 1A06.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF000036; ehand; 4.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD000001; Euk_pkinase; 1.
DR ProDom: PD000012; EF-hand; 2.
DR SMART: SM000054; EFh; 4.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS00018; EF-HAND; UNKNOWN_4.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 487 AA; 54700 MW; 54E6PF5D93AEB2 CRC64;

Query Match 67.5%; Score 1751; DB 10; Length 487;
Best Local Similarity 69.1%; Pred. No. 1e-120;
Matches 327; Conservative 64; Mismatches 80; Indels 2; Gaps 2;

QY 14 VLPYOTPLRDHYLLGKLGQSGFTTYLCTEKSTSANACKSIKPKLVCREYEDVWR 73
Db 12 VLGHKTPNRLDYALGRKLGGQSGFTTYLCTENSTNEYACKSISKRLKSDVEDVRR 71

QY 74 EIQIMHHLSEHPNVRIKGTYESVFEHIVMEVCEGGLFDRIYVSKGHFSEAEVAKLIKT 133
Db 72 EIQIMHHLAGKNIVTIKAYEDPLVHVIMELSGGELFDRIQGHYTERKAAELTKI 131

QY 134 ILGWVEACHSLGMVRDLKPNFLFDSPKDAKLKATDFGLSVFYKPGQYLYDVVGSPPY 193
Db 132 IVGWVEACHSLGMVRDLKPNFLVLLNKDDDFSLKAIDFGLSVFYKPGQYLYDVVGSPPY 191

QY 194 VAPEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETESICFRIQLQGLDKSDPWPTI 253
Db 192 VAPEVLKHYGPADVWTAGVILYLLSGVPPFWAETQGGIFDAVLKLGHIDFSDPWPLI 251

QY 254 SEAAKDLIVKMLERSPKKRISAHEALCHPWIVDEQAAPKPLDPAVLSRLKQFSOMNKIK 313
Db 252 SDGKDLIRKMLCSQSERITAHQVLCHPWICENGAVPADRAIDPAVLSRLKQFSAMNKLK 311

QY 314 KMALRVIAERLSSEIEGLKELFKMIDTNSGTITFEELKAGLRKVGSELMESEIKSLMD 373

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Db 312 KMALRVIAERLSSEIEGLKELFKMIDTNSGTITFEELKAGLRKVGSELMESEIKSLMD 371
QY 374 AADIDNSGTIDYIEFTAAFLHLNKLREHLLVAAPSYFDKDGSGYITVDELQACKEHN 433
Db 372 AADVRSKGTIDYIEFTAAFLHLNKLREHLLVAAPSYFDKDGSGYITVDELQACKEHN 431

QY 434 COTPLDDMIKEIDLDNDGKIDSEFTAMMRKGD-GVGRSRTMMKNLNFNIAD 485
Db 432 TDAFLIEDIIEVDQNDGRIDYGEFVAMTKGMVGVR-RTMRNSLNLSMRD 483

RESULT 11
O04123
ID O04123 PRELIMINARY; PRT; 554 AA.
AC O04123;
DT 01-JUL-1997 (Tremblrel. 04, Created)
DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Calcium-dependent protein kinase.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=INBRED LINE H84;
RX MEDLINE=97201047; PubMed=9048876;
RA Saijo Y., Hata S., Sheen J., Izui K.;
RT "cDNA cloning and prokaryotic expression of a maize calcium-dependent
RT protein kinase.";
RL Biochim. Biophys. Acta 1350:109-114(1997).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: D87042; BAA13232.1; -
DR HSSP: P02593; 1CTR.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF000036; ehand; 4.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD000001; Euk_pkinase; 1.
DR ProDom: PD000012; EF-hand; 2.
DR SMART: SM000054; EFh; 4.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS00018; EF-HAND; UNKNOWN_4.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 554 AA; 61056 MW; 51FC6F464684C57C6 CRC64;

Query Match 67.3%; Score 1745; DB 10; Length 554;
Best Local Similarity 70.0%; Pred. No. 3.4e-120;
Matches 333; Conservative 57; Mismatches 84; Indels 2; Gaps 2;

QY 13 TVLPYOTPLRDHYLLGKLGQSGFTTYLCTEKSTSANACKSIKPKLVCREYEDVWR 72
Db 78 SVLGHKTPNRLDYALGRKLGGQSGFTTYLCTENSTNEYACKSISKRLKSDVEDVRR 137

QY 73 EIQIMHHLSEHPNVRIKGTYESVFEHIVMEVCEGGLFDRIYVSKGHFSEAEVAKLIK 132
Db 138 EIQIMHHLGSGHTNVVAIKAYEDQLYVHVIMELCAGGELFDRIQGHYTERKAAELTR 197

QY 133 ILGWVEACHSLGMVRDLKPNFLFDSPKDAKLKATDFGLSVFYKPGQYLYDVVGSPPY 192
Db 198 IIVGWVEACHSLGMVRDLKPNFLVLLNKDDDFSLKAIDFGLSVFYKPGQYLYDVVGSPPY 257

QY 193 VAPEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETESICFRIQLQGLDKSDPWPTI 252
Db 258 VAPEVLKKNYGPADVWTAGVILYLLSGVPPFWAETQGGIFDAVLKLGHIDFSDPWPPV 317

QY 253 ISPAKDLIVKMLERSPKKRISAHEALCHPWIVDEQAAPKPLDPAVLSRLKQFSOMNKI 312

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Db 318 IDSADKLLIRMLNPRSAERLTAHEVLCHPWIRDHGVAEPDPLDPAVLSPRIKOFSAAMNKL 377
QY 313 KMALVIAERLSEEEIGGKELFKMIDTNSGTTITFEELKAGLRKVGSELMESEIKSLM 372
Db 378 KMALVIAESSEEEIAGLEKMFQMDTNSGAIYDELKEGLRYGSLTKDTEIRDLM 437
QY 373 DAADIDNSGTIDYGEFLAATLHNMKMEREEILVAAPSDFDKSGSYITIDELQSCTEFG 432
Db 438 DAADIDNSGTIDYGEFLAATLHNMKMEREEILVAAPSYDFDKSGSYITIDELQQAACKHN 497
QY 433 LCPDTPDDMTKEIDLNDGKIDSEBTAMMRKGD-GVGRSRTMMKNLNFNIADFG 487
Db 498 MPDAFLDDVINADQDNGRIDYGEFVAMTKGNMGVGR-RTMRNSLNTSMRDAPG 552

RESULT 12
ID Q38871 PRELIMINARY; PRT; 556 AA.
AC Q38871;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Calmodulin-domain protein kinase CDPK isoform 5.
GN CPK5 OR F23E12.130 OR AT4G35310
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Hrabak E.M., Dickmann L.J., Satterlee J.S., Sussman M.R.;
RA Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Bevan M., Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft A.,
RA Heiseil J., Jesse T., Heijnen L., Vos P., Mewes H.W., Mayer K.F.X.,
RA Schueller C.;
RA Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft A.,
RA Mewes H.W., Lemcke K., Mayer K.F.X.;
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RA submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RL -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; U31834; AAB03245.1; -
DR EMBL; AL022604; CAAL18738.1; -
DR EMBL; AL161587; CAB80248.1; -
DR HSSP; P02588; ITNX.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00036; ehand; 4.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 1.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 4.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_4.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 556 AA; 62127 MW; 737F1ADD582B45ED CRC64;

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Query Match 67.2%; Score 1742; DB 10; Length 556;
 Best Local Similarity 68.4%; Pred. No. 5.7e-120;

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Matches 329; Conservative 66; Mismatches 84; Indels 2; Gaps 2;
QY 6 NPPRPNTWLPYQTPLRDHYLLGKLGQGGTGYLCTEKSTKSANYACKSPKRLVCR 65
Db 77 NPDNQAYVYVGHKTPNIRDYITLSRKLGGQGGTGYLCTEKSTKSANYACKSPKRLVCR 136
QY 66 EYEDYWRREIQIMHLSSEHPNRYIKGTVEDSVFVHVMVEGEGELFQRIYSKGFHSER 125
Db 137 EYEDYWRREIQIMHLSSEHPNRYIKGTVEDSVFVHVMVEGEGELFQRIYSKGFHSER 196
QY 126 EAVKLLTKTIIGVVEACHSLGVMHRDLKPNFLFDSPKDDAKLKATDFGLSVFYKPGQYLY 185
Db 197 KAAELTKIIVGVVEACHSLGVMHRDLKPNFLLVNKDDDFSLKAIDFGLSVFYKPGQYLY 256
QY 186 DVVGSYYVAPEVVKCYGPEIDVWSAGVYLYILLSGVPPFWAETESGIFPROILQGLKDF 245
Db 257 DVVGSYYVAPEVVKCYGPEIDVWSAGVYLYILLSGVPPFWAETESGIFPROILQGLKDF 316
QY 246 KSDPWPTISEAAKDLIYKMLERSPKKRISAHEALCHFWIVDEQAAPDKPLDPAVLSRLKQ 305
Db 317 ESDPWPVVISDSADKLLRMLSSKPAERLTAHEVLRHPWICENGVAPODALDPAVLSRLKQ 376
QY 306 FQMNKIKKMAIRVIAERLSEEEIGGKELFKMIDTNSGTTITFEELKAGLRKVGSELME 365
Db 377 FSAMNKLKMAIKVIAESLSEEEIAGLEKMFQMDTNSGAIYDELKEGLRYGSLTKD 436
QY 366 SEIKSLMDAADIDNSGTIDYGEFLAATLHNMKMEREEILVAAPSDFDKSGSYITIDELQ 425
Db 437 TEHDLMDAADVNSGTYIDSEFLAATLHNMKMEREEILVAAPSDFDKSGSYITIDELQ 496
QY 426 SACTEFGLCDTPDDMTKEIDLNDGKIDSEBTAMMRKGD-GVGRSRTMMKNLNFNIAD 484
Db 497 QACVEHGMADVLEDDIIEKVDQNDGKIDYGEFVAMTKGNMGVGR-RTMRNSLNTSMRD 555
QY 485 A 485
Db 556 A 556

RESULT 13
Q93XJ0 PRELIMINARY; PRT; 578 AA.
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AC Q93XJ0;
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DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Calcium dependent protein kinase.
GN RICDPK1.
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. RISHIRI; TISSUE=SUSPENSION CULTURE;
RA Furuichi N., Okuta T., Hara N.;
RT "Calcium dependent protein kinase genes from resistant and susceptible
RT potato cultivars to Phytophthora infestans.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB051808; BAB63463.1; -
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00036; ehand; 4.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 1.
DR ProDom; PD000012; EF-hand; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_4.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
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KW ATP-binding; Kinase; Transferase.

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Job time : 80 secs
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GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 26, 2003, 08:35:21 ; Search time 5487 Seconds
(without alignments)
9266.011 Million cell updates/sec

Title: US-09-848-806-2
Perfect score: 1747
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Scoring table: IDENTIFY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*

- 1: gb_ba:*
- 2: gb_htg:*
- 3: gb_in:*
- 4: gb_om:*
- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pl:*
- 9: gb_pr:*
- 10: gb_ro:*
- 11: gb_sts:*
- 12: gb_sy:*
- 13: gb_un:*
- 14: gb_vi:*
- 15: em_ba:*
- 16: em_fun:*
- 17: em_hum:*
- 18: em_in:*
- 19: em_mu:*
- 20: em_om:*
- 21: em_or:*
- 22: em_ov:*
- 23: em_pat:*
- 24: em_ph:*
- 25: em_pl:*
- 26: em_ro:*
- 27: em_sts:*
- 28: em_un:*
- 29: em_vi:*
- 30: em_htg_hum:*
- 31: em_htg_inv:*
- 32: em_htg_other:*
- 33: em_htg_mus:*
- 34: em_htg_pln:*
- 35: em_htg_rod:*
- 36: em_htg_mam:*
- 37: em_htg_vrt:*
- 38: em_sy:*
- 39: em_htgo_hum:*
- 40: em_htgo_mus:*
- 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1747	100.0	1747	8	ATHCDPKB	D21806 Arabidopsis
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3	1515.8	86.8	1519	8	AY113986	AY113986 Arabidops
4	1202.4	68.8	1657	8	ATU31752	U31752 Arabidopsis
5	826.4	47.3	1754	8	GMU69173	U69173 Glycine max
6	803.6	46.0	1732	8	AB051809	AB051809 Solanum t
7	756.4	43.3	1768	8	AX077706	AX077706 Sequence
8	756.4	43.3	1768	8	SOXCADPK	M64587 Glycine max
9	744.2	42.6	1693	8	ATACDPK9	U20388 Arabidopsis
10	712.6	40.8	2036	8	ATU31835	U31835 Arabidopsis
11	706.2	40.4	1858	8	ATHATCDPK	D28582 Arabidopsis
12	698.4	40.0	2393	8	AB051808	AB051808 Solanum t
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14	688.4	39.4	1967	8	ATU31834	U31834 Arabidopsis
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16	666	38.1	2019	8	NTA344154	AY072801 Cucurbita
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19	652.2	37.3	1746	8	CPU90262	AJ344156 Nicotiana
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22	649	37.1	2214	8	AY072802	L14771 Arabidopsis
23	645	36.9	2214	8	ATHCALLIPR	D84408 Maize mRNA
24	643.4	36.8	1857	8	D84408	U31833 Arabidopsis
25	641.8	36.7	2142	8	ATU31833	AX077717 Sequence
26	629.8	36.1	2022	6	AX077717	U08140 Vigna radia
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ALIGNMENTS

RESULT 1

ATHCDPKB

LOCUS

DEFINITION

Arabidopsis thaliana mRNA for calcium-dependent protein kinase

(CDPK), complete cds.

1747 bp mRNA linear

PLN 05-FEB-1999

ACCESSION

D21806

VERSION

D21806.1

KEYWORDS

calcium-dependent protein kinase; ATCDPK2.

SOURCE

Arabidopsis thaliana (strain:Columbia) cDNA to mRNA.

ORGANISM

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 1747)

REFERENCE

Urao,T., Katagiri,T., Mizoguchi,T., Yamaguchi-Shinozaki,K.,

Hayashida, N. and Shinozaki, K.
 Two genes that encode Ca(2+)-dependent protein kinases are induced
 by drought and high-salt stresses in Arabidopsis thaliana
 Mol. Gen. Genet. 244 (4), 331-340 (1994)
 94359455
 2 (bases 1 to 1747)
 Shinozaki, K.
 Direct Submission
 Submitted (30-Oct-1993) Kazuo Shinozaki, Tsukuba Life Science
 Center, The Inst. of Physical and Chemical Res.; 3-1-1 Kohyadai,
 Tsukuba, Ibaraki 350, Japan (E-mail: sinozaki@erts1.riken.go.jp,
 Tel.: 0298-36-4359, Fax: 0298-36-9060)
 On Mar 22, 1996 this sequence version replaced gi:540482.

COMMENT

Location/Qualifiers

FEATURES

source

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/strain="Columbia"

/db_xref="taxon:3702"

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/evidence=experimental

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primer_bind

polya_site

1747

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BASE COUNT

ORIGIN

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 Best local Similarity 100.0%; Pred. No. 0;
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 DB 1141 GTCCGATCTCAACTGATGGAATCAGAAATCAAGTCTCTCATGATCGGCTGATATCGAC 1200
 QY 1201 AACAGTGGTACAATAGACTACGGAGAAATTCCTAGCAGCAACCTTACACATGACAGATG 1260
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RESULT 3						
AY113986	1519 bp mRNA linear PLN 31-MAY-2002					
LOCUS	Arabidopsis thaliana putative calcium-dependent protein kinase					
DEFINITION	(Atlg35670) mRNA, complete cds.					
ACCESSION	AY113986					
VERSION	AY113986.1					
KEYWORDS	FLI CDNA.					
SOURCE	thale cress.					
ORGANISM	Arabidopsis thaliana					
REFERENCE	1 (bases 1 to 1519)					
AUTHORS	Yamada, K., Banh, J., Chan, M.D., Chang, C.H., Chang, E., Dale, J.M., Deng, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.					
TITLE	Arabidopsis Open Reading Frame (ORF) Clones					
JOURNAL	Unpublished					
REFERENCE	2 (bases 1 to 1519)					
AUTHORS	Yamada, K., Banh, J., Chan, M.M., Chang, C.H., Chang, E., Dale, J.M., Deng, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.					
TITLE	Direct Submission					
JOURNAL	Submitted (16-MAY-2002) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA					
COMMENT	The RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL CDNA : 'RIKEN Arabidopsis Full-length CDNA'): Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.					
The Saik, Stanford, PGEC (SSP) Consortium members constructed and sequenced the PUNI (ORF) clones using the RAFL cDNAs: Yamada, K., Banh, J., Chan, M.M., Chang, C.H., Chang, E., Dale, J.M., Deng, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L., Chen, H., Cheuk, R., Jones, T., Karlin-Neumann, G., Kim, C., Lam, B., Lin, J., Miranda, M., Nguyen, M., Palm, C.J., Shinn, P., Southwick, A., Davis, R.W., Ecker, J.R. and Theologis, A.						
The Saik, Stanford, PGEC (SSP) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP /PGEC) contributed equally to this work as PIs.						
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ecotype: Columbia"

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CDS

1..1488

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BASE COUNT 448 a 279 c 366 g 426 t

ORIGIN

Query Match

Best Local Similarity 86.8%; Score 1515.8; DB 8; Length 1519;

Matches 1517; Conservative 0; Pred. No. 0;

Mismatches 2; Indels 0; Gaps 0;

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DB	61	CGATTAAAGATCATTTACCTTCGGGAAAAAGCTAGGCAAGCCAAATTTGAAACAAC	120
QY	187	TATCTGTGACAGAAATCAACCTCGCTAATTAGCTGCAATCGCTCCGAGGCGA	246
DB	121	TATCTGTGACAGAAATCAACCTCGCTAATTAGCTGCAATCGCTCCGAGGCGA	180
QY	247	AAGCTCGTGTGCGGAGGATACGAAGATGATGCGGTGAGATTTCAGATCATCATCAT	306
DB	181	AAGCTCGTGTGCGGAGGATACGAAGATGATGCGGTGAGATTTCAGATCATCATCAT	240
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DB	241	CTCTGAGCATCAAAATGTTGATAGATCAAGGACCTATGAGATTCGGTGTGTTGTT	300
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QY	427	CATTTTGTAGTGGGTGAAGCTGTCAAGCTTATTAAAGACGATTTCTGTTGTTGAGGCT	486
DB	361	CATTTTGTAGTGGGTGAAGCTGTCAAGCTTATTAAAGACGATTTCTGTTGTTGAGGCT	420
QY	487	TGTCATTTCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT	546
DB	421	TGTCATTTCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT	480
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DB	541	GGCAATATTATATGACGTAGTTGGAGTCCGCTACTACTGTTCCACCACGAGGTGCTAAG	600
QY	667	AAATGTTATGACCTGAAATAGATGTTGGAGTGGTGGTGTATCTCTACATTTTACTTC	726
DB	601	AAATGTTATGACCTGAAATAGATGTTGGAGTGGTGGTGTATCTCTACATTTTACTTC	660
QY	727	AGCGGTGTTCCCTCCCTCTGGGACAGACTGAGTCTGGGAATCTTTAGACAGATATTGCA	786
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DB	1021	ACAGACAACAGCGGACGATTACTTTTGAAGAGCTCAAGCGGTTTGAAGAGAGTCGGA	1080
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DB	1081	TCTGAAGTATGATGAATCAGAAATCAAGTCTCTCATGGATCGGCTGATATCGAACACGT	1140
QY	1207	GGTACAATAGACTACGGAGAAATTCCTAGCAGCAACCTTACACATGACACAGATGGAGA	1266
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QY	1567	CCAAATTTCTGTTTTTTT 1585	
DB	1501	CCAAATTTCTGTTTTTTT 1519	

RESULT 4

ATU31752

LOCUS

DEFINITION

4 (CPK4) mRNA, partial cds.

ACCESSION

ATU31752 1657 bp mRNA linear PLN 23-AUG-2001
Arabidopsis thaliana calmodulin-domain protein kinase CDPK isoform
4 (CPK4) mRNA, partial cds.
U31752


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VERSION      U31752.1  GI:1399266
KEYWORDS
SOURCE       Arabidopsis thaliana.
ORGANISM     Arabidopsis thaliana
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE    1 (bases 1 to 1657)
AUTHORS      Hrabak,E.M., Dickmann,L.J., Satterlee,J.S. and Sussman,M.R.
TITLE        Characterization of eight new members of the calmodulin-like domain
              protein kinase gene family from Arabidopsis thaliana
JOURNAL      Plant Mol. Biol. 31 (2), 405-412 (1996)
MEDLINE      96343943
PUBMED       8756605
REFERENCE    2 (bases 1 to 1657)
AUTHORS      Hrabak,E.M.
TITLE        Direct Submission
JOURNAL      Submitted (17-JUL-1995) Estelle M. Hrabak, Horticulture, University
              of Wisconsin, 1575 Linden Drive, Madison, WI 53706, USA
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    QY 195 CACAGAGAATCAACCTCGGCTAATACGCTGCAATCGATCCCGAAGCGAAGCTCGT 254
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RESULT 6
AB051809
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DEFINITION Solanum tuberosum RiCDPK2 mRNA for calcium dependent protein
ACCESSION AB051809
VERSION AB051809.1 GI:15289759
KEYWORDS Solanum tuberosum
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ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; eusterids I; Solanales; Solanaceae; Solanum.
1
Furuichi,N., Okuta,T. and Hara,N.
Calcium dependent protein kinase genes from resistant and
susceptible potato cultivars to Phytophthora infestans
unpublished
2 (bases 1 to 1732)
Furuichi,N. and Okuta,T.
Direct Submission
Submitted (25-NOV-2000) Naotaka Furuichi, Niigata university,
Agriculture; 2-8050, Igarashi, Niigata shi, Niigata ken 950-2181,
Japan (E-mail:nfuru@agr.niigata-u.ac.jp; Tel:81-25-262-7520(ex.7520),
URL:http://www.niigata-u.ac.jp; Fax:81-25-262-7520)
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DEFINITION Arabidopsis thaliana calcium dependent protein kinase mRNA,
complete cds.
ACCESSION U20388
VERSION 020388.1 GI:836937
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SOURCE Arabidopsis thaliana.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Rosidae; eurosoid II; Brassicales; Brassicaceae; Arabidopsids.
HONG, Y., TAKANO, M., LIU, C. M., GASCH, A., CHYE, M. L. and CHUA, N. H.
Expression of three members of the calcium-dependent protein kinase
gene family in Arabidopsis thaliana
Plant Mol. Biol. 30 (6), 1259-1275 (1996)
96311013
PUBLISHED 8704134
REFERENCE 2 (bases 1 to 1693)
AUTHORS Hong, Y.
DIRECT SUBMISSION
SUBMITTED (27-JAN-1995) Yan Hong, Institute of Molecular and Cell
Biology, National University of Singapore, 10 Kent Ridge Crescent,
Singapore, Republic of Singapore, 0511
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DEFINITION Arabidopsis thaliana calmodulin-domain protein kinase CDPK isoform 6 (CPK6) mRNA, complete cds.
ACCESSION U31835
VERSION U31835.1
KEYWORDS GI:1399274
SOURCE Arabidopsis thaliana.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1 (bases 1 to 2036)
Hrabak,E.M., Dickmann,L.J., Satterlee,J.S. and Sussman,M.R.
Characterization of eight new members of the calmodulin-like domain
protein kinase gene family from Arabidopsis thaliana
Plant Mol. Biol. 31 (2), 405-412 (1996)
96343943
MEDLINE
PUBMED
8756605
REFERENCE
2 (bases 1 to 2036)
Hrabak,E.M.
Direct Submission
Submitted (18-JUL-1995) Estelle Hrabak, Horticulture, University of
Wisconsin, 1575 Linden Drive, Madison, WI 53706, USA
JOURNAL
Location/Qualifiers
1. 2036
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DEFINITION	Arabidopsis thaliana mRNA for calcium-dependent protein kinase, complete cds.			
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VERSION	2.1			
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AUTHORS	1 (bases 1 to 1858)			
TITLE	Urao,T., Katagiri,T., Mizoguchi,T., Yamaguchi-Shinozaki,K., Hayashida,N. and Shinozaki,K.			
JOURNAL	An Arabidopsis thaliana cDNA encoding Ca(2+)-dependent protein kinase			
MEDLINE	Plant. Physiol. 105 (4), 1461-1462 (1994)			
REFERENCE	95062734			
AUTHORS	2 (bases 1 to 1858)			
JOURNAL	Shinozaki,K.			
REFERENCE	Unpublished			
AUTHORS	3 (bases 1 to 1858)			
TITLE	Shinozaki,K.			
JOURNAL	Direct Submission			
	Submitted (19-FEB-1994) Kazuo Shinozaki, Tsukuba Life Science Center, The Inst. of Physical and Chemical Res.; 3-1-1 Kohyadai, Tsukuba, Ibaraki 350, Japan(E-mail:sinozaki@rtcs1.riken.go.jp,			

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On Mar 10, 1996 this sequence version replaced gi:535778.
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QY 973 CTAAGCAGTTTCTCAATGAATAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 1032
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Db 1068 AGCTCTCAG 1127
QY 1093 AACAGCGGAGAGATTTTGAAGAGCTCAAGCGGTTTGAAGAGAGAGAGAGAGAGAGAG 1152
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QY 1393 AAGGAGATTTGATTTGACAAATGACGAGAGAGATCGATTTCTGGAGTTTACAGCAATGATG 1452
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Db 1548 AGAGATGTAGGCA 1562

RESULT 12
AB051808
LOCUS
DEFINITION Solanum tuberosum R1CDPK1 mRNA for calcium dependent protein
AB051808
ACCESSION
VERSION AB051808
KEYWORDS
SOURCE Solanum tuberosum (cultivar:Rishiri) suspension culture cdna to mRNA, clone lib:potato cv. Rishiri cdna.
ORGANISM Solanum tuberosum

Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

1
Furuichi, N., Okuta, T. and Hara, N.
Calcium dependent protein kinase genes from resistant and susceptible potato cultivars to Phytophthora infestans unpublished
2 (bases 1 to 2393)
Furuichi, N. and Okuta, T.
Direct Submission
Submitted (25-NOV-2000) Naitaka Furuichi, niigata university, Agriculture; 2-8050, Igarashi, Niigata shi, Niigata Ken 950-2181, Japan (E-mail:nfuru@agr.niigata-u.ac.jp).
URL:http://www.niigata-u.ac.jp, Tel:81-25-262-7520(ex.7520), Fax:81-25-262-7520)
1. 2393
Location/Qualifiers
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Best Local Similarity 65.1%; Freq. No. 1.2e-140;
Matches 1029; Conservative 0; Mismatches 551; Indels 0; Gaps 0;
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QY	570	GGCTACCGATTTTGGTTTGTCTGTCTCTATTAAGCCAGGACAAATATATATGACGTAGT	629
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QY	630	TGGAAGTCGTACTATGTTTGCCACGAGAGTGCCTAAGAAATGTTTATGGAACCTGAAATAGA	689
Db	1312	TGCGAGCCCATACTATGTGCGCACGAGAGTTCTCCGAAAACGTTATGGTCTCTGAAGCTGA	1371
QY	690	TGTGTCGAGTGCGGGTGTTATCCTCTACATTTTACTTCAGCGGTGTTCTCTCCCTTCGGC	749
Db	1372	TGTTTGGAGTGCCTGTTTATTTCTCTACATCTTATTAAGTGGAGTAGCTCTCTTCTGGC	1431
QY	750	AGAGACTGAGTCTGGAATCTTTAGACAGATATGCAAGGGAAGTTAGATTTTCAATCTGA	809
Db	1432	TGAATAGCAGAGGATATTTGACACAGTCTCTGCACGGTGATCTTGACTTCAAGTCAGA	1491
QY	810	CCCGTGGCTTACTATCTCAGAAGCTGCTAAAGATTTGATCTATAAAATGCTCGSAAAGAG	869
Db	1492	CCCATGGCCAAAGTATTTCAAGAGATGCAAAAGACTTGATGAGGAGATGCTCGTTGCGA	1551
QY	870	CCCCAAGAACGATTTCTTGCTCATGAAGCCTTGTTGTCACCCATGGATTTGTCGATGAACA	929
Db	1552	TCCGAGAGAGCTTTAACTGCACTGAAGTTTATGCCATCTTTGGGTACAAGTTGATGG	1611
QY	930	AGCAGCACGACAGAACGCTTTGATCCAGCAGCTTATCTGCTCTAAAGAGTTTCTCTCA	989
Db	1612	TGTGGCTCCCGATAAGCCTCTGATCTGCACTTCTGAGTAGAATGAGCAATTTTCTGCG	1671
QY	990	ANTGAATAGATTTAAGAAATGGCATTTACGGGTAAATCTCTCAGAGACTTTTCAGAGGAAGA	1049
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QY	1050	AATTTGGAGTCTGAAGGAATTTCTCAAGATGATAGACACACACAGCAGCGGAACGATTAC	1109
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QY	1110	TTTTGAAGAGCTCAAGCGGGTTTGAAGAGAGTCGGATCTGAACTGATGGAATCAGAAAT	1169
Db	1792	TTTTTGAGGAGCTCAAGAAAGGCTTAAACGATTTTGGCTCTAATCTGAAGGAGACCGAGAT	1851
QY	1170	CAGTCTCTCATGGGATGCGGCTGATATCGACACAGTGGTACATAGACTACGGAGAATT	1229
Db	1852	CTATGATCTTATCGGCGAGCTGAGCTTGTATACAGTGGGAACAATTTGATTATGTTGAATT	1911
QY	1230	CTTAGCAGCAACTTACATCATCAACAAGATGGAGAGACGAGATTTCTGGTGGCTGCATT	1289
Db	1912	TATAGCTGCACNTTACATATAGACAAATTTGAAGACAAGATCATCTTTTGTGCTGTTT	1971
QY	1290	TTCCGGACTTTGACAAAGCGAAGCGGTTATATACCATCGATCAGCTTCAGTCAGCTTG	1349
Db	1972	CTGTTACTTCGATAAGATGGAAGTGGCTACATCACTCCGGATGAGCTTCAACAGCTTG	2031
QY	1350	CACAGAGTTTGGTCTATGTATACACTCTTGGACGACATGATCAAGGAGATTTGATCTTGA	1409
Db	2032	TGAAGAAITTTGGCATTTGGGGATGTCCGATGGAGAAATGATCAGAGAAAGCTGACCAAGA	2091
QY	1410	CAATGAGGGAAGATCGATTTCTCGAGTTTACACCATGATGAGGAAGAGAGATGAGT	1469
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Qy	1470	TGGGAGAGCAGAACCAATGATGAGAGAACTTGAACATCTCAACATTCGTCTGATGCTTTGGAGT	1529
Db	2152	GCTAGGTGTGGCAGAAAGGCTAGAGCAVAGTTTTCAGCATTTGCATTCAGAGAAGCAGT	2211
Qy	1530	TGATGGTCAAAAATCTGATGACTGACTCATCTCTTCCACAANTTCGTGTTTTTTTCTC	1589
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Db	2272	CTTGTGGAATTTTCTCTT	2291
RESULT 13			
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DEFINITION	Nicotiana tabacum mRNA for calcium-dependent protein kinase 3 (cdpk3 gene).		PLN 03-NOV-2001
ACCESSION	AJ344155		
VERSION	AJ344155.1	GI:16215470	
KEYWORDS	calcium-dependent protein kinase; cdpk3 gene.		
SOURCE	common tobacco.		
ORGANISM	Nicotiana tabacum		
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REFERENCE 2	Romeis, T., Ludwig, A.A., Martin, R. and Jones, J.D. Calcium-dependent protein kinases play an essential role in a plant defence response		
JOURNAL	EMBO J. 20 (20), 5556-5567 (2001)		
MEDLINE	21481752		
PUBMED	11597999		
REFERENCE 3	2 (bases 1 to 2437)		
AUTHORS	Romeis, T.		
TITLE	Direct Submission		
JOURNAL	Submitted (16-AUG-2001) Romeis T., The Sainsbury Laboratory, John Innes Centre, Norwich, Colney Lane, Norfolk, NR4 7UH, UNITED KINGDOM		
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Best Local Similarity	65.1%	Pred. No. 2.6e-140;	Length 2437;
Matches 1028;	Conservative	0; Mismatches 552;	Indels 0; Gaps 0;
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Db	721	AGGAAGAANTTAGNCAAGGTCATTTTGGAACTACATTTAAATGTGTCGAAAGGCAAC	780
Qy	210	CTCCGCTAATTAGCGCTGCAATTCGATCCGAAAGGAAAGCTCGTGTCGCGAGATTAT	269
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Qy	270	CGAAGATGTATGGCGTGAGATTTCAGATCATGCATCATCTCTCAGCATCCAATGTGT	329
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Db	1021	TGAGCTTACTAGAGACTATTGTTGGAGTTGTAGAGCTTGTCAATCTCTTGGTGTCAATGCA	1080
Qy	510	TAGAGATCTCAAACCTCGAATTTCTGTTTGTATAGTCTCTAAAGATGATGCTAAGCTTAA	569
Db	1081	TCGTGATCTTAAAGCCGTAATAATTTCTCTTGTGTAACAGAGAGGATTCACCTCTCAA	1140
Qy	570	GGCTACCGATTTTGGTGTGCTGTCTCTATTAAGCCAGGACAAATTTATATGACGTAGT	629
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Qy	750	AGAGACTGAGTCTGGAATCTTTTAGACAGATATTGCAAGGGAAGTTAGATTTCAATCTGA	809
Db	1321	TGAAATAGCAAGGAATATTTTGAACAAGTCTCTGCACGCTGATCTGTGATTTACAGCTCAGA	1380
Qy	810	CCGCTGGCCTACTATCTCAGAAGCTGTAAAGATTGATCTATAAAATGCTCGAAAGGAG	869
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Qy	870	CCCCAAGAAAGCATTTCTGCTCATGAAGCCTTGTGTCAACCATGGATTTGTGATGAACA	929
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Db	1561	AATGAACAAGCTCAGAAATGGCTTTGAGAGTCAATTTGCTGAAAGCCTATCCGAAAGA	1620
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Db	1681	TTTTGAGGAGCTCAANGATGGGTTTAAACGATTTGGCTCTATCTGAAGGAGCTCCGAGAT	1740
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Db	1741	CTATGATCTTATGACGAGCGAGCTGACGTTTGATACAGTGGACAAATTGATTATGCTGAATT	1800
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QY	1350	CACAGAGTTTGGTCTATGATGATACACCTCTCGGACGACATGATCAAGGAGATGATCTTGA	1409
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QY	1410	CAATGACGGGAAGATCGAATTTCTCGGAGTTTACAGCAATGATGAGGAAGGAGATGGAGT	1469
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Db	2041	GCTAGGTGGTGGCAAGAAAGGCTCTAGACATAGTTTTCAGCATTTGGATTCAGAGAAGCAGT	2100
QY	1530	TGATGCTGAAAAATCTGATGACTGACTCATCATCTTCCACAAATTTCTGTTTTTTTCTC	1589
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Db	2161	CTTGTGGAAATTTTCTGTT	2180
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BASE COUNT 581 a 351 c 466 g 569 t

ORIGIN

Query Match 39.4%; Score 688.4; DB 8; Length 1967;

Best Local Similarity 67.2%; Pred. No. 1.7e-138;

Matches 974; Conservative 0; Mismatches 476; Indels 0; Gaps 0;

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Db 1160 TGGATCTGTGAGAATGTTGTTGCACCATAGACACTAGATCCAGCTGTTCTTCTCGT 1219
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Qy 1513 GCTGATGCTT 1522
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RESULT 15

AC007887/c

LOCUS

DEFINITION

AC007887

AC007887

AC007887.9

HTG.

KEYWORDS

ORGANISM

Arabidopsis thaliana.

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

Genomic sequence for Arabidopsis thaliana BAC F1504 from chromosome I, complete sequence.

AC007887.9 GI:8778333

HTG.

Arabidopsis thaliana.

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 158096)

Ecker, J.R.

Direct Submission

Submitted (22-JUN-1999)

Department of Biology, University of Pennsylvania, 38th Street and

Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA

2 (bases 1 to 158096)

Ecker, J.R.

Direct Submission

Submitted (04-OCT-1999)

Department of Biology, University of Pennsylvania, 38th Street and

Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA

3 (bases 1 to 158096)

Chen, R., Shinn, P., Brooks, S., Buehler, E., Chao, Q.,

Johnson-Hopson, C., Khan, S., Kim, C., Altati, H., Bei, B., Chin, C.,

Choi, J., Choi, E., Conn, L., Conway, A., Gonzalez, A., Hansen, N.,

Howing,B., Koo,T., Lam,B., Lee,J., Lenz,C., Li,J., Liu,A., Liu,J.,
Liu,S., Mukharsky,N., Nguyen,M., Palm,C., Pham,P., Sakano,H.,
Schwartz,J., Southwick,A., Thaveri,A., Toriumi,M., Vaysberg,M.,
Yu,G., Davis,R., Federspiel,N., Theologis,A. and Ecker,J.
Direct Submission
Submitted (28-JUN-2000) Arabidopsis thaliana Genome Center,
Department of Biology, University of Pennsylvania, 38th and
Hamilton Walk, Philadelphia, PA 19104-6018, USA
On Jun 28, 2000 this sequence version replaced gi:6007863.
This submission of BAC F1504 is shorter by 138 bases. The
original BAC had a Tn10 transposon insertion
(gb|J01829.1|trn101513) from E. coli located at the junction of
bases 18229 and 18230 of this submission.

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CDS

CDS

CDS

CDS

CDS

CDS

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Search completed: March 26, 2003, 10:42:01
Job time : 5868 secs

Result No.	Score	Query Match	Length	DB ID	Description
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4	756.4	43.3	1768	22	AAF74274
5	688.4	39.4	1671	21	AAC42934
6	652.6	37.4	2550	22	AAF74283
7	629.8	36.1	2022	22	AAF74285
8	597.4	34.2	3054	21	AAC45793
9	571.4	32.7	2334	22	AAF74277
					Arabidopsis CDPK2
					Arabidopsis CDPK4
					Arabidopsis thaliana
					Soybean calcium dependent
					Arabidopsis thaliana
					Cucurbita pepo cal
					Vigna radiata' calic
					Arabidopsis thaliana
					Rice calcium depend

RESULT 1	
ABA06021	
ID	ABA06021 standard; cDNA; 1747 BP.
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XX	ABA06021;
XX	
XX	08-MAR-2002 (first entry)
DT	
XX	
DE	Arabidopsis CDPK2 encoding polynucleotide SEQ ID NO 2.
XX	
KW	Arabidopsis; CDPK2; CDPK4; calcium dependent protein kinase
KW	disease resistance; agricultural; pathogen; crop yield
KW	fungicide; bactericide; nematocide; insecticide; viric
KW	transgenic; plant; enzyme; gene; ss.
XX	
OS	Arabidopsis thaliana.
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PF	04-MAY-2001; 2001WO-US14368.
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PR	05-MAY-2000; 2000US-201925P.
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PA	(GEO) GEN HOSPITAL CORP.
XX	

Sheen J;
WPI; 2002-062179/08.
P-PSDB; AAM48000.
Producing plant having increased disease resistance, comprises regenerating plant from a non-naturally occurring plant cell over-expressing a polynucleotide encoding a calcium dependent protein kinase polypeptide -
Dislosure; Fig 1; 44pp; English.
The invention relates to producing a plant having increased disease resistance, comprising providing a non-naturally occurring plant cell over-expressing a polynucleotide encoding a calcium dependent protein kinase (CDPK) polypeptide and regenerating a plant from the plant cell, where the CDPK polypeptide is expressed in the plant, increasing the resistance of the plant to disease as compared to a naturally-occurring plant. The method is useful for a variety of agricultural and commercial purposes including improving a plant's resistance against plant pathogens, increasing crop yields, improving crop and ornamental quality and reducing agricultural production costs. The method facilitates an effective and economical method for in-plant protection against plant pathogens, reducing or minimising the need for traditional chemical practices (e.g. application of fungicides, bactericides, nematocides, insecticides, or viricides) that are typically used by farmers for controlling the spread of plant pathogens and providing protection against disease causing pathogens. The method contributes to the production of high quality and high yield agricultural products, e.g. fruits, ornamentals, vegetables, cereals and field crops having reduced spots, blemishes and blotches that are caused by pathogens, agricultural products with increased shelf-life and reduced handling costs and high quality and yield crops for agricultural (e.g. cereal and field crops), industrial (e.g. oilseeds) and commercial (e.g. fiber crops) purposes. The present sequence is that of Arabidopsis thaliana CDPK2 of the invention.
Sequence 1747 BP; 516 A; 316 C; 392 G; 523 T; 0 other;
Query Match 100.0%; Score 1747; DB 24; Length 1747;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1747; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GATCGGGTACATATCTTCTTCTTCAAAATCGAGATCGAAGAGAACCAACAAAAA 60
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DB 661 CTAAGAAATGTTATGAGCTGAATAGATGTTGAGTGTGAGTGTCTGTTTCTTCTACAT 720
QY 721 TTAAGTCAAGGCTTCTTCTTCTGAGAGAGTGTCTGAAATCTTTAGACAGATA 780
DB 721 TTAAGTCAAGGCTTCTTCTTCTGAGAGAGTGTCTGAAATCTTTAGACAGATA 780
QY 781 TTCAAGGGAAGTAGATTTCAATCTGACCCGTGCTTACTTCTCAGAGTGTCTATAA 840
DB 781 TTCAAGGGAAGTAGATTTCAATCTGACCCGTGCTTACTTCTCAGAGTGTCTATAA 840
QY 841 GATTTGATCTATAAATGCTGAAAGAGGCCCCCAAGAACGCAATTTCTGCTCATGAAGCC 900
DB 841 GATTTGATCTATAAATGCTGAAAGAGGCCCCCAAGAACGCAATTTCTGCTCATGAAGCC 900
QY 901 TTGTGTCAACCATGATTTGCGATGAACAGAGCAGCAGCAAGCTCTTTGATPCAGCA 960
DB 901 TTGTGTCAACCATGATTTGCGATGAACAGAGCAGCAGCAAGCTCTTTGATPCAGCA 960
QY 961 GTCTTATCTGCTTAAGCAGTCTTCTCAATGAATTAAGAAATGCAATTTACG 1020
DB 961 GTCTTATCTGCTTAAGCAGTCTTCTCAATGAATTAAGAAATGCAATTTACG 1020
QY 1021 GTAATTTCTGAGAGATTTCTCAGAGGAAATTTGAGGCTCTGAAGAAATTTTCAAGATG 1080
DB 1021 GTAATTTCTGAGAGATTTCTCAGAGGAAATTTGAGGCTCTGAAGAAATTTTCAAGATG 1080
QY 1081 ATAGACACAGACACAGCGAGGATTTCTTTTGAAGCTCAAGCGGGTTTGAAGAGA 1140
DB 1081 ATAGACACAGACACAGCGAGGATTTCTTTTGAAGCTCAAGCGGGTTTGAAGAGA 1140
QY 1141 GTCGGATCTGAATGGAATCAGAAATCAAGTCTCTCATGATCGGCTGATATCGAC 1200
DB 1141 GTCGGATCTGAATGGAATCAGAAATCAAGTCTCTCATGATCGGCTGATATCGAC 1200
QY 1201 AACAGTGGTACATAGACTACGAGAAATTCCTAGCAGCAACCTTACATGACAAAGATG 1260
DB 1201 AACAGTGGTACATAGACTACGAGAAATTCCTAGCAGCAACCTTACATGACAAAGATG 1260
QY 1261 GAGAGAGAGAGATTTCTGTTGCTGATTTTCAAGCTTTTCAAGAGCGGCTTAT 1320
DB 1261 GAGAGAGAGAGATTTCTGTTGCTGATTTTCAAGCTTTTCAAGAGCGGCTTAT 1320
QY 1321 ATACCATCGATGAGCTTCAGTCAAGCTTCAAGAGATTTGTTGTTGATGATACCTCTG 1380
DB 1321 ATACCATCGATGAGCTTCAGTCAAGCTTCAAGAGATTTGTTGTTGATGATACCTCTG 1380
QY 1381 GAGGACATGATCAAGAGATTTGATTTGACATGACGGAAGATCGATTTCTCGGAGTTT 1440
DB 1381 GAGGACATGATCAAGAGATTTGATTTGACATGACGGAAGATCGATTTCTCGGAGTTT 1440
QY 1441 ACAGCAATCATGAGGAAAGAGATTTGAGTGGAGAGCAGAACCATGATGAAGACTTG 1500
DB 1441 ACAGCAATCATGAGGAAAGAGATTTGAGTGGAGAGCAGAACCATGATGAAGACTTG 1500
QY 1501 AACTTCAACATTTGATGCTTTTGGAGTTGATGTTGAGTGAAGAAATCTGATGACTCATC 1560
DB 1501 AACTTCAACATTTGATGCTTTTGGAGTTGATGTTGAGTGAAGAAATCTGATGACTCATC 1560

QY 1561 ATTCTTCACAAATTCGTTTTTTTCTTTTCTTTTAAATTCGTTATATATTTGAATTTAAT 1620
DB 1561 ATTCTTCACAAATTCGTTTTTTTCTTTTCTTTTAAATTCGTTATATATTTGAATTTAAT 1620
QY 1621 TCTAAGATACAAAATATATTCGCGTGTGTTTTTGGTTTCCCTTTTATTTTGTGATAT 1680
DB 1621 TCTAAGATACAAAATATATTCGCGTGTGTTTTTGGTTTCCCTTTTATTTTGTGATAT 1680
QY 1691 GAGCAACTTCTAAATTTTATCTCATATGATGATAATTTTGGCTTCATATATAAAGTTT 1740
DB 1691 GAGCAACTTCTAAATTTTATCTCATATGATGATAATTTTGGCTTCATATATAAAGTTT 1740
QY 1741 GAATTC 1747
DB 1741 GAATTC 1747
RESULT 2
ID ABA06022 standard; cDNA; 1657 BP.
XX ABA06022;
AC ABA06022;
XX
DT 08-MAR-2002 (first entry)
XX
DE Arabidopsis CDPK4 encoding polynucleotide SEQ ID NO 4.
XX
KW Arabidopsis; CDPK2; CDPK4; calcium dependent protein kinase; oilseed;
KW disease resistance; agricultural; pathogen; crop yield; ornamental;
KW fungicide; bactericide; nematocide; insecticide; viricide; cereal;
KW transgenic; plant; enzyme; gene; ss.
XX
OS Arabidopsis thaliana.
XX
FH Key
CDS 1..1506
FT /*tag= a
FT /product= "CDPK4"
XX
PN WO200184911-A1.
XX
XX 15-NOV-2001.
XX
XX 04-MAY-2001; 2001WO-US14368.
XX
XX 05-MAY-2000; 2000US-201925P.
XX
XX (GEO) GEN HOSPITAL CORP.
XX
XX Sheen J;
XX
XX WPI: 2002-062179/08.
XX P-PSDB: AAM48001.
XX
XX Producing plant having increased disease resistance, comprises
XX regenerating plant from a non-naturally occurring plant cell
XX over-expressing a polynucleotide encoding a calcium dependent protein
XX kinase polypeptide -
XX
XX Disclosure; Fig 2; 44pp; English.
XX
XX The invention relates to producing a plant having increased disease
XX resistance, comprising providing a non-naturally occurring plant cell
XX over-expressing a polynucleotide encoding a calcium dependent protein
XX kinase (CDPK) polypeptide and regenerating a plant from the plant
XX cell, where the CDPK polypeptide is expressed in the plant, increasing
XX the resistance of the plant to disease as compared to a
XX naturally-occurring plant. The method is useful for a variety of
XX agricultural and commercial purposes including improving a plant's
XX resistance against plant pathogens, increasing crop yields, improving
XX crop and ornamental quality and reducing agricultural production costs.
XX The method facilitates an effective and economical method for in-plant

CC protection against plant pathogen, reducing or minimising the need for
CC traditional chemical practices (e.g. application of fungicides, typically
CC bactericides, nematocides, insecticides, or viricides) that are
CC used by farmers for controlling the spread of plant pathogens and
CC providing protection against disease causing pathogens. The method
CC contributes to the production of high quality and high yield agricultural
CC products, e.g. fruits, ornamentals, vegetables, cereals and field crops
CC having reduced spots, blemishes and blotches that are caused by
CC pathogens, agricultural products with increased shelf-life and reduced
CC handling costs and high quality and yield crops for agricultural
CC (e.g. cereal and field crops), industrial (e.g. oilseeds) and commercial
CC (e.g. fiber crops) purposes. The present sequence is that of Arabidopsis
CC thaliana CDPK4 of the invention.
XX
SQ Sequence 1657 BP; 500 A; 287 C; 384 G; 486 T; 0 other;
Query Match 68.8%; Score 1202.4; DB 24; Length 1657;
Best Local Similarity 84.1%; Pred. No. 1.6e-262;
Matches 1384; Conservative 0; Mismatches 251; Indels 11; Gaps 2;
QY 75 GAAGCCAAACCCCTAGACGTCCTTCAACACACAGTTCTACCATATCAACACACGATTAA 134
DB 6 GAAACCAAACCCCTAGAGACCCCTCAACACAGTTCTTCCATACGAAACACCAAGATTAA 65
QY 135 AGATCAATTACCTTCGGGAAAAAAGCTAGGCCAAGSCCAATTTGGAACAACCTATCTCTG 194
DB 66 AGATCACTATCTCTCGGCAAAAGCTAGGCCAAGSCCAATTTGGAACAACCTATCTCTG 125
QY 195 CACAGAGAAATCAACCTCGGCTAATTAGCCCTGCAAAATCGATCCGGAAGCGAAAGCTCGT 254
DB 126 TACAGAGAAATCATCATCAGCTAATACGCTTGCAATCAATCCCAAAACGTAAGCTTGT 185
QY 255 GTGCGCGAGGATTACGAGATGTATGGCGTGAGATTGAGATCATGATCATCTCTCTGA 314
DB 186 ATGCTGTGAAGACTACGAGATGTATGGCGTGAGATTGAGATCATGATCATCTCTCTGA 245
QY 315 GCATCAAAATGTTTAGCATCAAGGGGACTTATGAAGATTCGGTGTGTTGTTTCATATCT 374
DB 246 GCATCCTAATGTTGTAGAAATCAAGGGTACTTATGAAGACTCTGTTTGTTCATCTCT 305
QY 375 TATGGAGTTTGTGAAGTGGTGAGCTTTTGTATCGGATTTTCTTAAGGTCATTTTATG 434
DB 306 TATGGAGTTTGTGAAGTGGTGAGCTTTTGTATCGGATTTTCTTAAGGTTGTTTATG 365
QY 435 TGAGCGTGAAGCTGTCAAGCTTATTAAGACGATCTTGGTGTGTTGTTGAGCGTTGTCATTC 494
DB 366 TGAACCGTGAAGCTGTCAAGTGTATTAAGACTATCTTGGTGTGTTGTTGAGCGTTGTCATTC 425
QY 495 TCTTGTGTTTATGCATAGAGATCTCAACCTGAGAAATTTCTTGTGTTGATGTCCTAAAGA 554
DB 426 TCTTGTGTTTATGCATAGAGATCTTAAAGCTGAGAAATTTCTTGTGTTGATGTCCTAAAGA 485
QY 555 TGATGCTAAGCTTTAAGCTACCGATTTTGGTTTGTCTGCTCTTATTAAGCGAGGACAATA 614
DB 486 TGATGCTAAGCTTTAAGCTACAGACTTTGGTTTGTCTGCTCTTATTAAGCGAGGAGTA 545
QY 615 TTTATATGAGCTAGTTGGAAGTCCGTAATATGTTGCACAGAGTGTCTTAAGAAATGTTA 674
DB 546 TCTGTATGATGTTAGTTGGAAGTCCGTTATATGTTGCACCTGAGGTTCTTGAAGAAATGTTA 605
QY 675 TGGACCTGAAATAGATGTGTTGAGTGTGTTGTTATCTCTACATTTTACTACGCGTGT 734
DB 606 TGGACCAAGATAGAGATGTGTTGAGCGCGGTGTATCTTGTACATCTTACTAAGTGGGT 665
QY 735 TCCTCCCTTCTGGCGAGAGACTGAGTCTGGAATCTTTTAGACAGATATTTGCAAGGAGTT 794
DB 666 TCCTCCCTTCTGGCGAGAAACCCGAGTCAGGAATCTTTAGGCAGATATTTGCAAGGAGAT 725
QY 795 AGATTCAAAATCTGACCCGTGGCTTACTATCTCAGAGCTGCTTAAGATTTGATCTATAA 854
DB 726 AGATTTTAAATCTGATCCGTGGCTTACTATCTCAGAGGTCGTAAGATTTGATTTACAA 795
QY 855 AATGCTGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 914


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PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142377.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
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PR 09-AUG-1999; 99US-0147493.
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PR 11-AUG-1999; 99US-0148319.
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PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
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PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.

PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
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PR 07-OCT-1999; 99US-0158029.
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PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 67.7%; Score 1183.2; DB 21; Length 1506;
Best Local Similarity 88.2%; Pred. No. 3.5e-258;
Matches 1287; Conservative 0; Mismatches 173; Indels 0; Gaps 0;

QY 75 GAAGCCAAACCCCTAGAGTCCTTCAACACAGTTCTACCATATCAACACACAGGATTAAG 134
DB 6 GAAACCAACCCCTAGAGACCCCTCAACACAGTTCTTCCATAGCAACACCAAGATTAAG 65
QY 135 AGATCATTACCTTCTGGGAAAAAGCTAGGCCAAGCCAAATTTGGAACACACCTATCTCTG 194
DB 66 AGATCATTATCTCTCGGCAAAAGCTAGGCCAAGCCAAATTTGGAACACCTATCTCTG 125
QY 195 CACAGAGAAATCAACCTCCGCTAATTTACGCTGCAATCGATCCCGAAGCGAAAGCTCT 254
DB 126 TACAGAGAAATCATCATCAGTAAATFACGCTTGCAATCAATCCCAAAACGTAAGCTTCT 185
QY 255 GTGTCGCGAGGATTACGAAGATGTATGGCGTGAGATTCAGATCATCATCTCTCTGA 314
DB 186 ATGTCGTGAAGACTAGCAAGATGTATGGCGTGAGATTCAGATCATCATCTCTCTGA 245
QY 315 GCATCCAAATGTTGTTAGGATCAAGGGACTTATGAAGATTCGCTGTTGTTTCATATCT 374
DB 246 GCATCCTAAAGTTGTTAGAAATCAAGGTTACTTATGAAGACTCTGTTTTGTTTCATATCT 305
QY 375 TATGAGGTTTGTGAGGTGGTGGAGCTTTTGTGATCGGATTTGTTCTAAAGGTCATTTAG 434
DB 306 TATGGAAGTTTGTGAGGTGGTGGAGCTTTTGTGATCGGATTTGTTCTAAAGGTCATTTAG 365
QY 435 TGAGCGTGAAGCTGTCACGCTTATTAAGACGATTCCTTGGTGTGTTGAGGCTTGCTATTC 494
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Db ` 1446 TGAAGCTTTTGGAGTTGAGG 1465

RESULT 4
AAAF74274

ID AAF74274 standard; DNA; 1768 BP.

XX AC AAF74274;

XX DT 04-MAY-2001 (first entry)

XX DE Soybean calcium dependent protein kinase clone #2.

XX DE Calcium dependent protein kinase; CDPK; herbicide resistance;
KW paraquat; diquat; crop production; ds.
XX OS Glycine max.
XX PN WO200107592-A2.
XX PD 01-FEB-2001.
XX PF 26-JUL-2000; 2000WO-GB02876.
XX PR 27-JUL-1999; 99GB-0017642.
XX PA (ZENE) ZENECA LTD.
XX PI Holt CD, White AJ, Michael AJ, Osborn RW;
XX PS WPI; 2001-168549/17.
XX PT Producing herbicide resistance plants by inhibiting calcium dependent
PT protein kinase in plants or by providing an intracellular vacuolar
PT transporter capable of transporting agrochemical into plant vacuole
XX Claim 18; Page 37; 50pp; English.
XX The present invention describes a method of producing plants which are
CC resistant to the herbicides paraquat and diquat involving inhibiting
CC the plants a calcium dependent protein kinase (CDPK) and selecting the
CC plants which are resistant to the agrochemical of interest. This is
CC useful in the production of crops with herbicide resistance.
XX Sequence 1768 BP; 511 A; 325 C; 464 G; 468 T; 0 other:

Query Match 43.3%; Score 756.4; DB 22; Length 1768;
Best Local Similarity 70.6%; Pred. No. 1.6e-161;
Matches 1009; Conservative 0; Mismatches 421; Indels 0; Gaps

QY 106 GTTCATCATATCAACACCACGATTAAAGAGATCAITTAACCTCTCGGAAAAAAGCTAGGC 165
| | | | | | | | | | | | | | | | | | | | | |
Db 195 GTTCTCCGCGAGCGCAGACAATCCGTGAGTGTAACGAGTTGGCGGAAGCTCGGG 254
| | | | | | | | | | | | | | | | | | | | | |
QY 166 CAAGGCCAATTTGAACAACCTATCTCTGCACAGAGAAATCAACCTCCGCTAATTACGCC 225
| | | | | | | | | | | | | | | | | | | | | |
Db 255 CAGGCCCCAATTCGGGACCACTTCGAGTGCACGCGCGTGCAGAGTGSTGGGAAGTTTCGGG 314
| | | | | | | | | | | | | | | | | | | | | |
QY 226 TGCAATTCGATCCCGAAGCAAAGCTGCTGTGCGGAGGATTACGAAGAATGATATGCGGT 285
| | | | | | | | | | | | | | | | | | | | | |
Db 315 TGCAAGTCGATTCGGAAGCGGAAGCTGCTGTGCAAGGAGGACTACGAGGACGTGTGCGG 374
| | | | | | | | | | | | | | | | | | | | | |
QY 286 GAGATTGAGATCATCATCTCTGTGACATCCAAAATGTTGTTAGGATCAAAAGGACT 345
| | | | | | | | | | | | | | | | | | | | | |
Db 375 GAGATTGAGATTAATGACCACTTGTTCGGAACACGCCAACCTTCCGCGATCGAAGGGACG 434
| | | | | | | | | | | | | | | | | | | | | |
QY 346 TATGAAGATCCGGTGTGTTGTCATATTTATGAGGTTTTGTCGAAGTGTGTGAGCTTTTT 405
| | | | | | | | | | | | | | | | | | | | | |
Db 435 TAGAGGATTCACGGCGGTGCACCTGGTCATGAGTTGTGCAGGGTGGAGAGTTGTT 494
| | | | | | | | | | | | | | | | | | | | | |
QY 406 CATCGGATGTTTCTAAAGTTCATTTTAGTGAGCGTGAAGCTGTCAAGCTTAATAAGAGC 465
| | | | | | | | | | | | | | | | | | | | | |
Db 495 GACAGGATTCGTGCAGAGGGACACTACACGAGAGACAGCGCGGAGTTGATAAGAGCG 554
| | | | | | | | | | | | | | | | | | | | | |

Qy 466 ATTCTTGCTGTTGTTAGGCTTGTCATCTCTTGTTGTTGTTATGCTATGAGATCTCAAACT 525
Db 555 ATTTGTTGAGTTGTTGAGGCTGTCACCTGCTAGGCTGTCATGAGGACCTTAAGCCT 614
Qy 526 GAGAAATTCCTGTTGTTAGTTCCTTAAGATGATGCTAGCTTAAGCTACCGATTTGGT 585
Db 615 GAGAAATTCCTGTTGTTAGTTCCTTAAGATGATGCTAGCTTAAGCTACCGATTTGGT 674
Qy 586 TTGCTGCTTCTTAAGCCAGGCAATATTATATGATGCTAGTGTGGAAGTCCGACTAT 645
Db 675 TTGCTGCTTCTTAAGCCAGGCAATATTATATGATGCTAGTGTGGAAGTCCGACTAT 734
Qy 646 GTTGACACAGAGTCTTAAGAAATTTATGACCTGAAATAGATGTGGAGTCTGGT 705
Db 735 GTTGACACAGAGTCTTAAGAAATTTATGACCTGAAATAGATGTGGAGTCTGGT 794
Qy 706 GTTATCTCTTCAATTTTACTCAGCGGTGTTCTCTCTCTGCGGACAGACAGTCTGCTGA 765
Db 795 GTTATCTCTTCAATTTTACTCAGCGGTGTTCTCTCTCTGCGGACAGACAGTCTGCTGA 854
Qy 766 ATCTTTAGACAGATTTCAAGGGAAGTTAGATTTCAATCTGACCCGTGGCTACTATC 825
Db 855 ATCTTTAGACAGATTTCAAGGGAAGTTAGATTTCAATCTGACCCGTGGCTACTATC 914
Qy 826 TCAGAAGCTGCTAAGATTTGATCTATATAATGCTCGAAGAGGCCCCAAGAACGCAIT 885
Db 915 TCAGAAGCTGCTAAGATTTGATCTATATAATGCTCGAAGAGGCCCCAAGAACGCAIT 974
Qy 886 TCTGCTCAATGAGGCTTGTGTCACCCATGATGTTGCGATGAACAGACAGCAGACAG 945
Db 975 ACAGCAGATGAGTACTCGGCCACCCATGATGTTGCGATGAACAGACAGCAGACAG 1034
Qy 946 CTTCTTGATCAGAGCTTCTATCTGCTTAAGCAGTTTCTCAAAATGAATTAAG 1005
Db 1035 CTTCTTGATCAGAGCTTCTATCTGCTTAAGCAGTTTCTCAAAATGAATTAAG 1094
Qy 1006 AAAATGGCATTACGGGTAATTCCTGAGAGCTTTCAAGAGGAAATTTGGAGGCTGAAG 1065
Db 1095 AAAATGGCATTACGGGTAATTCCTGAGAGCTTTCAAGAGGAAATTTGGAGGCTGAAG 1154
Qy 1066 GAAATGTTCAAGATGATAGACACAGACAAACGGAAGCTTACTTTTCAAGAGCTCAA 1125
Db 1155 GAAATGTTCAAGATGATAGACACAGACAAACGGAAGCTTACTTTTCAAGAGCTCAA 1214
Qy 1126 GCGGTTTGAAGAGCTGCGGATCTCAACTGATGGAATCAGAAATCAAGTCTCTATGGAT 1185
Db 1215 GCGGTTTGAAGAGCTGCGGATCTCAACTGATGGAATCAGAAATCAAGTCTCTATGGAT 1274
Qy 1186 GCGGCTGATATCGACAGCTGTTACATAGACTACGAGAAATCTTAGCAGCAACCTTA 1245
Db 1275 GCGGCTGATATCGACAGCTGTTACATAGACTACGAGAAATCTTAGCAGCAACCTTA 1334
Qy 1246 CACATGACAGATGGAGAGAGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1305
Db 1335 CACATGACAGATGGAGAGAGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1394
Qy 1306 GACGAGCGGTTATATCACTGATGCTTCACTGATGCTTCACTGATGCTTCACTGATGCT 1365
Db 1395 GACGAGCGGTTATATCACTGATGCTTCACTGATGCTTCACTGATGCTTCACTGATGCT 1454
Qy 1366 TGTATACACCTCTGAGAGATGATCAAGGAGATGATCAATGAGGAGGAGATC 1425
Db 1455 TGTATACACCTCTGAGAGATGATCAAGGAGATGATCAATGAGGAGGAGATC 1514
Qy 1426 GATTTCTCGAGTTTACAGCAATGATGAGAAAGAGATGAGTGGGAGAGCAGAAC 1485
Db 1515 GATTTCTCGAGTTTACAGCAATGATGAGAAAGAGATGAGTGGGAGAGCAGAAC 1574
Qy 1486 ATGATGAGAACTTCACTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1535
Db 1575 ATGATGAGAACTTCACTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1624

RESULT 5

AA42924
ID AAC42924 standard; DNA; 1671 BP.
XX
AC AAC42924;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 37370.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123160.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 16-APR-1999; 99US-0128714.
PR 19-APR-1999; 99US-0129845.
PR 21-APR-1999; 99US-0130077.
PR 23-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 04-MAY-1999; 99US-0132407.
PR 05-MAY-1999; 99US-0132484.
PR 06-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
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PR 20-MAY-1999; 99US-0135124.
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PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.

Db	963	TATATGTCTGTGGAGAGCGCAACTGGGAAGAGTATCCTTGTAGTCTATGTCAAAGAGG	1022
QY	247	AAGCTCGTGTCGCGCAGGATTAGCAAGATATATGGCGTGAGATTAGATCATCAGATCAI	306
Db	1023	AAGTTGGTTAATGAGGATCATCTTCAAGATCTGAGAAGGGAATTCAGATAATGCACCAT	1082
QY	307	CTCTCFAGCATCCAAATGTTGTTRAGGATCAAAAGGACTATAGAGATTCGGTGTTTGGT	366
Db	1083	TTTCTTGGACACCCGAATGTTATATPCGATCAAGGGGCGTACGAGGATCGCGTTGCAGTT	1142
QY	367	CATATTGTTATGAGAGTTTGTGAAGTGGTCAGCTTTTGTGATCGGATGTTTCTTAAAGGT	426
Db	1143	CAGGTAGTCATGGAGTTGTGTCTGGAGGTGAGCTATTGTGATAGGATCATTCACGTTGGA	1202
QY	427	CATTTTAGTGAGCGTCAAGCTGTCAAGCTTTATTAAGACGATCTTGGTGTTGTGAGCCT	486
Db	1203	CATTATACGGAAGAAAGGCTCTCGAGCTTACTAGGACCATAGTTCGGGGTTTGGAGGCA	1262
QY	487	TGTCATCTCTTGGTGTATGATAGATGATCTCAAACCTGAGAATTTCTTGTTTGATAGT	546
Db	1263	TGTCAGCTCTTGGAGTTATGCACCGTGACCTTAGCCCGAGAAATTTCTCTTTGTAGC	1322
QY	547	CCTAAAGATGATGCTAAGCTTAAGGCTACCGAATTTTGGTTGTCTGCTCTCTATAAGCCA	606
Db	1323	AAGGAAGAGGAATCACTTCTCAAGCAATGATGTTTGACATCAATGTTCTTCCAACCA	1382
QY	607	GGACAATATTATATCAGCTAGTTCGAAGTCGCTACTATGTTGCACAGAGTGCTAAAG	666
Db	1383	GGCGAAAGTTTAATGATGTGGTCGGAGTCCGTACTATGTTGCACCTGAAGTTTTCGGG	1442
QY	667	AAATGTTATGGAOCTGAATATAGATGTGTGGAGTGCTGTGTGTATTCCTTACATTTTACTC	726
Db	1443	AAGCGATATGGTCCAGAAGCAGATGTTTGGAGTGTGGAGTAATGTATACATTCCTGTTA	1502
QY	727	AGCGGTGTCCTCCCTCTTGGCCAGAGCTGAGTCTGGAATCTTTAGACATATTCGAA	786
Db	1503	AGTGGAGTGCCTCCCTTTTGGGCTGAGTCTGAGGAAGGATATTTGAAGAGTCCCTGCAC	1562
QY	787	GGGAAGTTAGATTTCAAATCTCACCCGTGGCCCTACTATCTCAGAGCTGCTTAAAGATTG	846
Db	1563	GGCGATCTTGACTTCTCCTCCGACCCTTGGCCACGATCTCGACAGTGCAGAAAGATTG	1622
QY	847	ATCTATRAAATGCTCAAGAGGCCCCAGAAAGCATTTCTGCTCATGAGACCTTGTGT	906
Db	1623	GTTAGAAGAATGTTGTGAGACCCGGAAGAGACACTGACAGCATATGAAGTTTGTGTC	1682
QY	907	CACCCATGAGTTCTCGATGAACAAGCAGCACCAAGCCCTCTTGATCCAGCAGCTGTTA	966
Db	1683	CACCTTGGCTTCAAGTTGATGGTGTGCTCTGACAGCCGCTTGACTCGGCAGTCTTG	1742
QY	967	TCCTGCTAAAGCAGTTTTCTCAATGAATAGATTAAGAAATGGCATTCAGGGGTAAAT	1026
Db	1743	ACTCGCTTGAAGCAGTTTTCAGCCATGAAACAAGCTCAAGAAATGGCTATCAAGGTCAIT	1802
QY	1027	GCTCAGAGACTTTCAGAGGAAGAAATGGAGGTCTCAAGGAATGTTCTCAAGATGATAGAC	1086
Db	1803	GCAGAGAGCTTATCTGAGGAAGAAATGCTGGAATCTCAAGGAATGTTCAAGATGATAGT	1862
QY	1087	ACAGACAACAGCGGAACGATTACTTTTGAAGAGCTCAAAAGCGGGTTTGAAGAGAGTCGGA	1146
Db	1863	ACTGACAACAGCGCCAAATCACATTTGAAGAACTCAAAGCTGGATGAAAGAGTTTGGGA	1922
QY	1147	TCTGAATGATGGAATCAGAAATCAAGTCTCTCATGGATCGCGGCTGATATCGACAACAGT	1206
Db	1923	GCTAATCTTAAGGAGTCCGAAATTTACGACCTTAATCGAAGCAGCGGATATAGACAACAC	1982
QY	1207	GGTCAATATAGACTACGAGAGATTCCTTAGCAGCAACCTTACACATGAACAAGATGAGAGA	1266
Db	1983	GGAAACATCGACTACGGGGAGTTCTGTAGTGCACATTCGATCTTAAACAAATCGAGAG	2042
QY	1267	GAGGAGATTTCTGGTGGCTGCAATTTTCGGACTTTGACAAAGACGGAAGCGGTTATATCACC	1326

Db	2043	GAGATCATCTTCTAGCAGCGTTTTCATATTTTCGCAAGAAGATGGNAGCGGTTTCATTACC	2100
Qy	1327	ATCGATGAGCTTCAGTCAGCTTCACAGAGTTTGGTCTATGTGATACACCTCTCGAGAC	1386
Db	2103	CACGACGAGCTTCAACAAGCATGTAAGAGTTTCGGGATAGAGGATCTTCAATGGAGAA	2162
Qy	1387	ATGTCACAGCAGATTCATCTTGACATGACGGGAAGATCGATTTCTCGAGCTTTACAGCA	1446
Db	2163	ATGATGGCGAGTTCGATCAACAACATGACGGAAGCATCGACTATACGAGTTCTGTGGG	2222
Qy	1447	ATGATGAGGAAAGGAGATGGAGT	1469
Db	2223	ATGATGCAAAAAGGAAATGTAGT	2245
RESULT 7			
AAAF74285			
ID	AAAF74285 standard; DNA; 2022 BP.		
XX	AAAF74285;		
XX	04-MAY-2001 (first entry)		
XX	Vigna radiata calcium dependent protein kinase clone.		
XX	Calcium dependent protein kinase; CDPK; herbicide resistance;		
KW	paraquat; diquat; crop production; ds.		
XX	Vigna radiata.		
XX	WO200107592-A2.		
XX	01-FEB-2001.		
XX	26-JUL-2000; 2000WO-GB02876.		
XX	27-JUL-1999; 99GB-0017642.		
XX	{ZENNE } ZENECA LTD.		
PA	Holt CD, White AJ, Michael AJ, Osborn RW;		
PI	WPT; 2001-168549/17.		
DR	Producing herbicide resistance plants by inhibiting calcium dependent		
XX	protein kinase in plants or by providing an intracellular vacuolar		
PT	transporter capable of transporting agrochemical into plant vacuole		
XX	Claim 18; Page 44-45; 50pp; English.		
XX	The present invention describes a method of producing plants which are		
CC	resistant to the herbicides paraquat and diquat, involving inhibiting		
CC	the plants a calcium dependent protein kinase (CDPK) and selecting those		
CC	plants which are resistant to the agrochemical of interest. This is		
CC	useful in the production of crops with herbicide resistance.		
XX	Sequence 2022 BP; 587 A; 374 C; 466 G; 595 T; 0 other;		

Query Match	36.1%	Score 629.8;	DB 22;	Length 2022;
Best Local Similarity	65.3%	Pred. No. 7.5e-133;		
Matches 925: Conservative	0:	Mismatches 492;	Indels 0;	Gaps 0

Qy	116	ATCAAAACACCACGATTAAAGAGATCATTAAGCTTCTGGGAAAAAGCTAGGCCAAGCCCAAT	175
Db	140	ATAAGATCCCACATTCGTGTGATCTATACACTCTTGGCCGCAATTTGGACACAGGACAAT	199
Qy	176	TTGGAACAACCTATCTCTGCACAGAGAAATCAACCTCCGCTAATTAACGCTTCGAATCGA	235
Db	200	TTGGCACCACTTATTTATGACCCAGAAATTCACCTTCCAAATGAATATGCTTCGAATCTA	259
Qy	236	TCCGGAAGCGAAAGCTGCTGTGTGCGCGAGATTAACGAAGATATGTCGCTGAGATTCAGA	295
Db	260	TCTCCAAAGAAAGATTCGATTTCCAAAGGAGGATCTCAGAGATTCAGAGGGGAAATTCAGA	319

xx The present invention describes a method of producing plants which are
cc resistant to the herbicides paraquat and diquat, involving inhibiting in
cc the plants a calcium dependent protein kinase (CDPK) and selecting those
cc plants which are resistant to the agrochemical of interest. This is
cc useful in the production of crops with herbicide resistance.

Sequence 2022 bp: 587 A: 374 C: 466 G: 595 T: 0 other; XX

Query Match	Score	DB	Length
36.1%	629.8	DB 22	Length 2022

Query Match
Best Local Similarity
65.3%; Pred. No. 7.5e-133;

Matches 925; Conservative 0; Mismatches 492; Indels 0; Gaps 0;

116 ATCAAAACACCAAGATTAAAGAGATCATTACCTTCTGGGAAAAAAGCTAGGCCAAGGCCAAT 175

QY II8 AICAAACACCAGATTAAGAGATCATTACCTTCGCGAATAAGCATACCCCAACGCCCAAT

Db 140 ATAAGACTCCCAACATTCGTGATCTATACACTCTTGGCCGCAATTTGGACAGGACAAT 199

[illegible]

QY 176 TTGGAAACAACCTATCTCTGCACAGAGAAATCAACCTCCGCTAATTACGCCCTGCAAAATCGA 235

db 200 TTGGCACCACTTATTTATGCACCGAGAA TTCTACTTCCAATGAATATGCCTGCAAAATCTA 259

DD IIGCCACCTTATTTATGCCCCCGGGATTCTACCTCCAGTCGATTTCCTCCTCCTTCTCTT

Z00 TIGGCACCTTATTTATGCCCCCGGGATTCTACCTCCAGTCGATTTCCTCCTCCTTCTCTT

QY 236 TCCCGAAGCGAAAGCTCGTGTGTCGCGAGGATTACGAAGATGTATGCGGTGAGATTGAGA 295

310

Qy	296	TCATGCCATCATCTCTCTGAGCATCCAAATGTTGTTAGGATCAAGGGACTTATGAAGATT	355
Db	320	TAATGCATCATTTAGCTGGTCACAAGAACATTTGCACANTRAGGTCCTTACGAGATC	379
Qy	356	CGGTGTTTGTTCATATGTTTATGAGAGTTTGTGAAGTGGTGAGCTTTTGTATCGGATTG	415
Db	380	CTCTCTATGTGCATATAGTCATGAGACTTTGCTTGGGGTGAGTTGTTTGAICGCATCA	439
Qy	416	TTTCTAAAGTGTCATTTAGTGACGCTGAGCTGCAAGCTTATTAAGACGATCTCTGGTG	475
Db	440	TCACAGGGCCACTATACCGAGGAAGGCTGACAGTTGACCAAAATTAATTTGGGG	499
Qy	476	TTGTTGAGGCTTGTCAATCTCTTGTGTTTATGCATAGAGATCTCAAACCTCAGAAATTC	535
Db	500	TTGTTGAGGCTTGTCAATCCCTTGGSGTCAATGCACAGAGATCTCAAGCCAGAAAACITTC	559
Qy	536	TGTTTGATAGTCTTAAGATGATGCTTAAGCTTAAGGCTACCGATTTTGGTTTGTCTGTCT	595
Db	560	TTTGTGTCATAAAGATGATGATTTCTCTCTTAAAGCAATTGACTTTGGCCTCTCCGTTT	619
Qy	596	TCATTAAGCCAGGACAAATATTTATATGACGTAGTTGGAAGTCGGTACTATGCTCCACAG	655
Db	620	TCITCAACCCGGTCAAAATTTCACTGATGTAATCGGCAGGCCATCTATGTTGCTCCTG	679
Qy	656	AGGTGCTAAAGAAATGTTATGGACCTGAAATAGATGTGTGGAGTGTCTGGTGTATCTCT	715
Db	680	AGSTTCTCTCAAGCACTATGGCCCTGAAGCAGACGTGTGGACAGCGGTGCTCATACTGT	739
Qy	716	ACATTTTACTACGGGTGTCTCCCTTCTGGCAGAGACTGAGTCTGGAACTTTTAGAC	775
Db	740	ACATATTGCTTAGTGTACCAACCAATTTGGCAGAGACCCACAAGGTAATATTGATG	799
Qy	776	AGATATTGAAGGAAAGTTAGATTTCAAATCTCAACCGTGGCTACTATCTCAGAAGCTG	835
Db	800	CAGTATTGAAGGACATATAGATTTTGACTCAGATCCCTTGGCTCTAATACTCACAGTG	859
Qy	836	CTAAGATTGATCTATAAATGTCTCGAAGAGAGCCCAAGAACGATTTCTGCTCATG	895
Db	860	CAAAAGATCTGATCAGAAAGATGCTGTGTCTCAAGCTTCAGAGCGTTGACTGCTCATC	919
Qy	896	AAGCCTTGTCTACCCATGGATTTGCGATGAACAAGCAGACACCAAGCAAGCTCTTGATC	955
Db	920	AAGTGTATGTCATCTTGATATGTGAATAATGGASTTTGCACCTTGACAGGCAATAGACC	979
Qy	956	CAGAGCTTATCTCTCTAAAGCAGTTTCTCAAAATGAATAAGATTAAAGAAATGGCAT	1015
Db	980	CTGCTGTCTTCTCTGCTCTAAACAGTTTCTTGCATGAATAAGCTGAAGAAGATGGCAT	1039
Qy	1016	TACGGGTAAATGCTGAGACACTTTCAGAGGAAGAATTTGAGGTCTGAAGAAATTTGTCA	1075
Db	1040	TGCGGGTGATGCTGAAAGCTATCTGAGAGAGGATTTCTGGATTGAGAGAAATGTTTC	1099
Qy	1076	AGATGATAGACAGACACACAGCGGACGATTTCTTTTGAAGAGCTCAAAGCGGTTTGA	1135
Db	1100	AGCCTATGGAATCCGATAACAGTGGTGAATCACATTTTGTATGAATCAAAAGCTGGTCTAA	1159
Qy	1136	AGAGAGTCGATCTGAACCTGATGGAATCAGAAATCAAGTCTCTCATGGATCGGCTGATA	1195
Db	1160	GAGATATGGTTCTACCCCTTAAGATGTAGAATAACGTGATCTGATGGAACGGCTCATG	1219
Qy	1196	TCGACACAGTGTACAAATAGACTACGGAGAATTCCTAGCAGCAACCTTACACATGAACA	1255
Db	1220	TCGACAAAGTGCACCAATAGATTATGGGAGCTTTATTTGCTCTACAGTCTCATCAACA	1279
Qy	1256	AGATGGAGACAGAGAGATCTGTGGTGGCTGCATTTCTGGAGCTTTGACAAGACGGAAGC	1315
Db	1280	AACCTAGACCTGAAGAACATCTTATTCAGCACTTCCAAATATTTTGACAAGGATGGCAGT	1339
Qy	1316	GTTATATCACCATCGATGAGCTTCAGTCAAGCTGTCACAGAGTTTGGTCTATGTATACAC	1375
Db	1340	GTTATATACGGTTGATGACTTTCACAAGCTTTGTGCAGAACATAACATGACTGATGCTT	1399

Qy	1376	CTCTGGACGACATGATCAAGGAGATTGATCTTCACAAATGACGGGAGAGATCGATTCTCGG	1433
Db	1400	TTCTTGAAGATATNTTATAGGGAAGTTGATCAGATATATGATGGAAGATGATATATGGTG	1459
Qy	1436	AGTTTACAGCAANTGATGAGGAAGAAGAGATGGATGGGGAAGACAGACCAATGATGAAGA	1495
Db	1460	AATTTGTGCAATGATGCAAAAGAACCAATGCTGGAAATTTGGTAGGAGGACTATGGCCAATA	1519
Qy	1496	ACTTGAACTTCAACATGTGCTGATGCTTTGGGAGTTGA	1532
Db	1520	GTCTGGAATTTAAAGCATGAGGGAGCGCATCTAGTGTCTCA	1556

RESULT 8	
AAC45753	
ID	AAC45753 standard; DNA; 3054 BP.
XX	
XX	
AC	
AC	AAC45753;
XX	
DT	18-OCT-2000 (first entry)
XX	
DE	Arabidopsis thaliana DNA fragment SEQ ID NO: 47639.
XX	
XX	
KW	Hybridisation assay; genetic mapping; gene expression control;
KW	protein identification; signal transduction pathway;
KW	metabolic pathway; promoter; termination sequence; ss.
XX	
XX	
OS	Arabidopsis thaliana.

PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
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PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
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PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
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PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 34.2%; Score 597.4; DB 21; Length 3054;
Best Local Similarity 63.6%;
Matches 947; Conservative 0; Mismatches 506; Indels 36; Gaps 1;

QY	63	AAAAATGGAGACGAAGCCAAAACCCCTAGACGTCCTTTCAAACACACAGTTTACCATATCAAAAC	122
Db	1554	ACATATGAGGAGAGTGTCCAGTGCAGGGCTTAGAACTCAGTCACTGTTGCAGAGGAAAAC	1613
QY	123	ACCACGATTTAAGNATCATACCTTCTGGGAAAAAGCTAGGCCAAGGCCAAATTTGGAAC	182
Db	1614	TGAAAACCTTTAAGGAGTCTATTTCATTAGGGAGGAACTTGGACAAGGCCAAATTTGGGAC	1673
QY	183	AACTATCTCTGCACAGAGAAATCAACCTCCGCTAAATACGCCCTGCAAAATCGATCCCGAA	242
Db	1674	GACGTTTTATGCCITGAAAGGTTACTGGGAACGAATATGGGTGCAAGTCGATTTCCAA	1733
QY	243	GCAAAAGCTGCTGTGTGCGCGAGGATACAGAGATGTATGGCGTGAGATTCAGATCATGCA	302
Db	1734	GAGGAAGCTTTTGACTGATGAGGATGTTGAAGATGTGAGAAGAGAGATTCAGATAATGCA	1793
QY	303	TCATCTCTGAGCATCCAAAATGTTGTAGGATCAAAAGGACTTATGAAGATTCGGGTGT	362
Db	1794	TCACTTGGCTGGTCATCCGAATGTTATATCTATTAAGAGTGCTTATGAGGATGTTGTGC	1853
QY	363	TGTTCAATTTGTTATGAGGTTTTGTGAAGTGGTGAGCTTTTTGATCGGATTTGTTCTAA	422
Db	1854	GGTACATCTTGTGATGAGTGTGTTGCGGTGGCGAGCTTTTTTGATAGAAATTTCAACG	1913
QY	423	AGTCAATTTTAGTGACGTHGAACTGTCAAGCTTTAAGACGATCTTGGTGTGTTGA	482
Db	1914	TGACATTTACACTGAGAGAAAAGCTGCTGAGCTTCGGAGAACCATTGTGGGGTTTTAGA	1973
QY	483	GGCTTGTCATCTCTTGTTGTTATGCATAGACATCTCAAACTGAGAAATTTCTTGTTGA	542
Db	1974	GGCTTGGTCATCTCTTGTTGTTATGCATCGGACCTCAAGCCAGAGAAATTTCTATTTGT	2033
QY	543	TAGTCTTAAAGATGCTGAAGCTTAAGCTTACCAGTTTGGTTGCTGCTCTCTATAA	602
Db	2034	TAGTAGAGGAAATCTCCCTGTGAAAACGATGACATTTGGACTCTCAATGTTCTTTAA	2093
QY	603	GCAGGACAAATTTTATGAGCTAGTTGGAGTCCGTACTATGTTGCACACAGAGTGCT	662
Db	2094	GCAGATGAGGTTTTTACAGATGTTGTGGTAGTCGCTATTATGTAGCTCCAGAAGTTCT	2153
QY	663	AAAGAAATGTTATGGACCTGAAATAGATGTGGGAGTGTGGTGTATCCCTCTACATTTT	722
Db	2154	TAGAAAGCGTTAATGGTCCCTGAATCAGATGTGTGGATGCTGGTGTGATTTGTACATTTT	2213
QY	723	ACTCAGGTTGTTCTCCCTCTCTGGG-----	748
Db	2214	GTTAAGCGGAGTTTCCCTCTTTTCTGGCGCGCTCTGAACTAAATTTGTTTCCATGAATA	2273
QY	749	--CAGAGACTGAGTCTGGAATCTTTAGACAGATATTGCAAGGGAAGTTAGATTTCAAATC	806
Db	2274	TACAGAACCGAACAGGTTATTTTCGAGCAGGTCCTTCATGGAGATCTTGACTTTTCATC	2333
QY	807	TGACCGCTGGCCTACTATCTCAGAAGCTGCTTAAGATTTGATCTATAAAATGCTCGAAG	866
Db	2334	TGATCCATGGCCCAAGCATCTCTGAAAGCGGAAAGACTTGGTAAGGAAAATGCTTTGTTCG	2393
QY	867	GAGCCCCAAGAACGATTTCTGCTCATGAAAGCTTGTGTCACCCATGGATTTGTCATGA	926
Db	2394	AGACCCCAAGCGAAGACTAACCGCATCAAGATATATGTCTATCCATGGGTACAGATTGA	2453
QY	927	ACRAGACGACCAAGAACGCTCTTCATCCAGCAGTCTTATCTCGTCTCTAAAGCAGTTTC	986
Db	2454	CGGTGTGGCTCCAGATAAACCTCTGACTCTGCTGTCTGAGCCGATGTCAGCAATTTTC	2513
QY	987	TCAATGAATTAAGATTAAGAAAATGGCATTTACGGGTAAATTGCTGAGAGACTTTCAGAGGA	1046
Db	2514	TGCAATGAACAAGTTCAAGAAAATGGCTCTTAGAGTCTATAGCTGAGAGCTTATCTGAAGA	2573
QY	1047	AGAAATTTGAGGTTCTGAAGGAATTTGTTCAAGATGATAGACACAGACACACGCGGAACGAT	1106
Db	2574	AGAAATAGCCGGTTTTAAACAAATGTTTCAAGATGATAGACGAGACAAATAGTGGTTCAGAT	2633

Qy	1107	TACTTTTGAAGAGACTCAAGCGGGTTTGAAGAGAGATCGGATCTGAACCTGATGGAAATCAGA	1163
Db	2634	CACCTTTTGAAGAACTGAAAGCAGGAGCTAAAGACGAGTTGGTGCCTAATCTCAAGAGATCAGA	2693
Qy	1167	AATCAAGTCTCTCATGGTCCGGCTGATATCGACAAACAGTGGTACAAATAGAGACTACGGAGA	1226
Db	2694	GATTTCTGATCTTAATGCAAGCTGCTGATGTGGCACAATACGGGAACGATAGACTACAAAGA	2753
Qy	1227	ATTCTTAGCAGCAACCTTACATCAATCAACGAAGATGGAGAGAGAGGAGATTTCTGGTGGCTGC	1286
Db	2754	GTTCATAGCGCCACATTCATCTAAACAAATAGAGAGAGAGGACCATTTGTTTCGCCGC	2813
Qy	1287	ATTTTCGGACTTTTGCAAAAGACGGAAGCGGTTATATCACCAATFCATGAGCTTCAGTCAGC	1346
Db	2814	CTTCTCTTACTTTTGACAAGSAGCAGAGAGTGGCTTTATCACCCCGACGAGCTTCAACAGC	2873
Qy	1347	TTGACAGAGTTTGGTCTATGTGATACACCTCTGGACGACATGATCAAGAGAGATTGATCT	1406
Db	2874	TTCCGAAGAGTTTGGTCTTGAGATGCCCGCAATAGAGAAATGATGCCCGATGTTGATCA	2933
Qy	1407	TGCAATTAGCGGGAAGATCGATTTCTCGGAGTTTACAGCAATGATGAGGAAAGGAGATGG	1466
Db	2934	AGACAAGGATGGAGCAATAGACTACCAACGAGTTTGTGCAATGATGACAGAAAGGAGCAT	2993
Qy	1467	AGTTGGGAGAGCAGAACCAATGATGAAGAACTTGAACATTCACATTGCT	1515
Db	2994	AATGGGAGGACCTGTGAAGATGGGTTTAGAGAACAGCATTTAGCATTTCT	3042
RESULT 9			
AAF74277			
ID AAF74277 standard; DNA; 2334 BP.			
XX	AC	AAF74277;	
XX	AC		
XX	DT	04-MAY-2001 (first entry)	
XX	DE	Rice calcium dependent protein kinase clone #1.	
XX	KW	Calcium dependent protein kinase; CDPK; herbicide resistance;	
XX	KW	paraquat; diquat; crop production; ds.	
XX	XX		
OS		Oryza sativa.	
XX	XX		
XX	XX	WO200107592-A2.	
XX	PD	01-FEB-2001.	
XX	XX		
XX	PF	26-JUL-2000; 2000WO-GB02876.	
XX	PR	27-JUL-1999; 99GB-0017642.	
XX	XX	(ZENE) ZENECA LTD.	
XX	PA		
XX	XX		
PI		Holt CD, White AJ, Michael AJ, Osborn RW;	
XX	XX		
XX	DR	WPI; 2001-168549/17.	
XX	XX		
PT		Producing herbicide resistance plants by inhibiting calcium dependent	
PT		protein kinase in plants or by providing an intracellular vacuolar	
PT		transporter capable of transporting agrochemical into plant vacuole	
XX	PS	Claim 18; Page 39; 50pp; English	

The present invention describes a method of producing plants which are resistant to the herbicides paraquat and diquat, involving inhibiting in the plants a calcium dependent protein kinase (CDPK) and selecting those plants which are resistant to the agrochemical of interest. This is useful in the production of crops with herbicide resistance.
 Sequence 2334 BP; 659 A; 430 C; 625 G; 620 T; 0 other;

Query Match	Score	DB	Length
32.7%	571.4	22	2334

Best Local Similarity 62.2%; Pred. No. 1.3e-119; Matches 899; Conservative 0; Mismatches 546; Indels 0; Gaps 0;

Qy 91 COTCCTTCAACACAGCTTCTACCATATCAACACACACAGATTAAGAGATCAATACCTCTG 150
 Db 531 COTCATCTATCAATGCTCTGGGGGAGACACGGGACCTTAAGGAGCATTAATCAT 590
 Qy 151 GGAANAAGCTAGGCGCAAGGCAATTTGGACACAGCTATCTCTGACAGAGAAATCAACC 210
 Db 591 GGTGGGAAGCTTGGTCAGGCCAGTTTGGCACAACTTACCTCTGTACCGAGATCAATACA 650
 Qy 211 TCCGCTAATAGCCCTGCAATCGATCCGAGCGAAGAGCTCGTGTGCGGAGGATTAAC 270
 Db 651 GGGTGTGAGTATGCTTGAAGACCAATCCAAAGCGCAAGCTCATCCAAAGGAGATGTA 710
 Qy 271 GAAGATGTATGCGGTGAGATTCAGATCATCTCTCTGACATCCCAAAATGTTGT 330
 Db 711 GAAGATGTGCGCGGTGAGATTCAGATCATCTCTCTGCGGCCACAAAGATGTTGT 770
 Qy 331 AGGATCAAGGAGCTTATGAAGATTCGGGTGTTTGTTCATATTTATGAGAGTTTGTGA 390
 Db 771 GCAATCAAGGATGCTATGAGGATGGCAAGCGGTGCACATTTGTATGAGGCTCTCGCT 830
 Qy 391 GGTGTGAGCTTTGATCGGATGTTCTTAAGGTCTATTTAGTGAGGTGCAAGCTGTC 450
 Db 831 GGTGGGAGCTCTTTGACAGGATTCAGGAGAGGGCAITACAGGCGGAGGAGCTGCA 890
 Qy 451 AAGCTTATTAAGACGATCTTGGTGTGTGAGGCTTGTCTCTCTCTGTTGTTATGCAAT 510
 Db 891 GAGCTTATTAAGATTAATGTCAGCATTTGGTGTGTCATTCGTCGCAITTCGTCGGGTGATGCAC 950
 Qy 511 AGAGATCTCAACCTGAGATTTCTTTGTTGATGATCTCTTAAGATGATGCTAGCTTAAG 570
 Db 951 CGTGATCTTAAGCCAGAAATTTCTCTCTTGGTAAAGATGATGATCTGTCAATTAAG 1010
 Qy 571 GCTACGATTTGGTGTGCT 630
 Db 1011 GCAATGATTTGGTGTGCT 1070
 Qy 631 GGAAGTCCGCTACTATGTCACACAGAGGTGCTAAAGAAATGTTATGAGCTCAAAATAGAT 690
 Db 1071 GGGAGTCCATATATCTCTCTCTGAGTATTGCACAAACGTTATGACAGCAATCTGAT 1130
 Qy 691 GTGTGAGTCTGCTGTTATCT 750
 Db 1131 GTGTGAGTCTGCTGTTATCT 1190
 Qy 751 GAGACTGAGTCTGGAATCTTACACAGATATTGCAAGGAAAGTTAGATTTCAATCTGAC 810
 Db 1191 GAGACACACAGGATATTGATGAGTCTCTGAGGTCACATTTGATTTCAATCTGAT 1250
 Qy 811 CCGTGGCTACTATCTCAGAGCTGCTAAAGATTTGATCTATAAATGCTCGAAAGAGC 870
 Db 1251 CCATGCCAAAGATATCTGACAGTGAAGAGATCTTATAGAAAATGCTCTCTCTCTG 1310
 Qy 871 CCCAAGAGGCTTTCTGCTCAGAGCTGCTGTCACCCATGAGTTGTCGATGAACAA 930
 Db 1311 CCTTCGAGGCTTTGAAGGCCCATTAAGTCTTAAGGCTATCCCTTGGATCTGTAATGGA 1370
 Qy 931 GCAGCACACAGAGCTCTTGTATCCAGCATCTTATCTCTCTCTCTCTCTCTCTCTCTCTCT 990
 Db 1371 GTTGGCACTGATCAAGCTCTGGATCCAGGTTATCTCTCTCTCTCTCTCTCTCTCTCTCT 1430
 Qy 991 ATGATTAAGATTAAGAAATGCTTACGGGTAATGCTGAGAGCTTTTTCAGAGGAAGA 1050
 Db 1431 ATGAAAGATTAAGAAATGCTTCTGAGAGTATGATGAGGCTCTTTCAGAGGAGGAG 1490
 Qy 1051 ATTGGAGCTGAGGAGATTTGTTCAAGATGATGACACAGACACAGGCAAGATTAAT 1110
 Db 1491 ATTGCTGGTTAAGAGAAATGTTCAAGGAGTGGACACAAATAAGGTGTAATCACT 1550
 Qy 1111 TTTGAGAGCTCAAGCGGTTTGAAGAGAGTCGGATCTGAATCTGATGGAATCAGAAATC 1170

Db 1551 TTCGCTGAGCTTAGAGAGGTTTAAAGAGATTTGGCGCTGAATTTAAGGATACAGAGATT 1610
 Qy 1171 AAGTCTCTCATGGATGGGCTGATATCGACAAACAGTGGTACAAATAGACTACGGGAATTC 1230
 Db 1611 GGTGATATAATGGAGCGGCACACACGCAATATATTAACAATCCATTAATGAAGAATTT 1670
 Qy 1231 CTACGACAACTTACACATGAACAAGATGGAGAGAGAGATCTGCTGGCTGCAATTT 1290
 Db 1671 ATTGCTGCAATCTACCTCTTAACAAGATGAAGCTGAGGAGACCTCTGCGAGCTTTT 1730
 Qy 1291 TCGGACTTTGACAAAGACGAGGAGGTTTATATCACCATTCGATGAGCTTCAGTCAAGCTTGC 1350
 Db 1731 ACATATTTTGACAAAGATGGGAGTGGTGTATATCACAGTTGACAAAGCTTCAACGAGCTTGT 1790
 Qy 1351 ACAGAGTTTGGTCTATGATACACCTCTGACGACATGATCAAGAGATTTGACTTGCAC 1410
 Db 1791 GGAGAACATACATGAGGAGTTCCTCTCTGAAGAGATTTTTCAGAGGTTGATCAAAAC 1850
 Qy 1411 AATGACGGAAGATGATTTCTCGGAGTTTACAGCAATGATGAGGAAAGGAGATGGAGTT 1470
 Db 1851 AATGACGCGCAATTTGACTACCGCAATTTGTAGCCATGATGCAAGGAGCAACGTTGGA 1910
 Qy 1471 GGGAGAGCAGAACCAATGATGAGAACTTGAACCTTCAACATTTGATGCTGCTTTTGGAGTT 1530
 Db 1911 CTAGGTTGGCAACAATGGAAGCAGTTTGAATGTAGCATTAAGAGAGCGCACCTCAAGTA 1970
 Qy 1531 GATGG 1535
 Db 1971 CATTTG 1975

RESULT 10
 AAF74275
 ID AAF74275 standard; DNA; 1910 BP.
 XX
 AC AAF74275;
 XX
 DT 04-MAY-2001 (first entry)
 XX
 DE Sweet potato calcium dependent protein kinase clone.
 XX
 KW Calcium dependent protein kinase; CDPK; herbicide resistance;
 KW paraquat; diquat; crop production; ds.
 XX
 OS Ipomoea batatas.
 XX
 PN WO200107592-A2.
 XX
 PD 01-FEB-2001.
 XX
 PF 26-JUL-2000; 2000WO-GB02876.
 XX
 PR 27-JUL-1999; 99GB-0017642.
 XX
 PA (ZENE) ZENECA LTD.
 XX
 PI Holt CD, White AJ, Michael AJ, Osborn RW;
 XX
 DR WPI; 2001-168549/17.
 XX
 PT Producing herbicide resistance plants by inhibiting calcium dependent
 PT protein kinase in plants or by providing an intracellular vacuolar
 PT transporter capable of transporting agrochemical into plant vacuole
 XX
 PS Claim 18; Page 38; 50pp; English.
 XX
 CC The present invention describes a method of producing plants which are
 CC resistant to the herbicides paraquat and diquat, involving inhibiting in
 CC the plants a calcium dependent protein kinase (CDPK) and selecting those
 CC plants which are resistant to the agrochemical of interest. This is
 CC useful in the production of crops with herbicide resistance.
 XX
 SQ Sequence 1910 BP; 560 A; 348 C; 481 G; 521 T; 0 other;

Query Match 30.7%; Score 537.2; DB 22; Length 1910;
Best Local Similarity 63.2%; Pred. No. 6.8e-112;
Matches 843; Conservative 0; Mismatches 488; Indels 3; Gaps 1;

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OY 131 TAAGAGATCATTTACCTTCCTGGGAAAAGAGTAGGCCAAGCCCAATTTGGAAACACCTATC 190
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 308 TTAGGCGCATTTACACTCTGGGAAAGAACTGGGTAGGGGTCAATTTGGGGTTTACCTATT 367
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 191 TCTGCACAGAAATCAACTCGCTCAATTTACGCCCTGCAAAATCGATCCGGAAGCGAAAGC 250
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 368 TGTCTACTGAGATTGAAGTGAAGAGTATGCTTGCCTGCAAGTCAATTTCCAGAAAGAGC 427
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 251 TCGTGTCTCCGAGGATTACGAAGATGTATGGCGTGAGATTTCAGATCATGCAATCTCT 310
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 428 TTGTGACTAAGGGGATAAGGATGATATGAGGAGGAGGTTTCAGATTATGCGACACTTGA 487
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 311 CTGAGCATCCAAATGTTGTAGGATCAAGGGGACTTATGAAGATTCGGTGTGTTTCATA 370
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 488 GTGGCAGCCTATATTTGTAGTTCAAGGGGCTTATGAGGATGCTAATCTCTGTATC 547
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 371 TTTTATGAGGTTTCTGAAGGTGTCGAGCTTTTTCGATCGATTGTTTCTAAAGGTCAIT 430
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 548 TTCTGATGAGTTGTCTGTGCTGGAGAGCTTTTCGATCGGATTATTGCTAAGGGCACT 607
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 431 TTAGTGCAGCTGAAGCTGTCAGCTTATTAAGACGATTCCTTGTGTTGTTGAGGCTTGTC 490
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 608 ATAGCGAAAGGGCTGCTGCTCTCTTTGTCAGGTCTTATAGTGAATGTTGTTTCATCTGCC 667
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 491 ATTCTCTGTTGTTATGCTAGAGACTCAAACTCAGAAATTTCTGTTTGTAGTACCTTA 550
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 668 ATTTTATGGCGTATGTCACCGGATTTGAAGCCCGAGAAATTTCTGTTGCTCTGATAAAA 727
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 551 AAGATGATGCTAAGCTTAAGGCTACCGATTTTGTGTTGCTCTCTCTAATAAGCCAGGAC 610
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 728 CTGAAATGCTGCTTGAAGGCTACTGATTTTGGCTTATCAGTGTTCATTGAAGAAGGAA 787
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 611 AATATTATATGATGAGTGTGAGTCCGCTACTATGTTGCACAGAGGCTCTAAAGAAAT 670
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 788 GGGTGTATAAGGATTTAGTGGGAGGCTTACTATGTTGCTCCGAGGCTTGGGGAGAA 847
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 671 GTTATGACCTGAAATAGATGCTGGAGTCTGCTGTTATCTCTACATTTTACTCAGCG 730
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 848 AGTATGGGAGGAGCGGATTTTGGAGTCCAGTCTTAATGTTCTATATTTACTCAGTG 907
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 731 GTGTTCTCCCTCTCGGCGAGAGCTGAGTCTGGAATCTTTAGACAGATTTGCAAGGGA 790
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 908 GTGTCCTCCCTCTCTGGGCTGAAACTGAGCGGGGATCTTTAATGCTATACTTTAAAGGAG 967
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 791 AGTTAGATTTCAATCTGACCCGTGGCTACTATCTCAGAGAGCTGCTAAAGATTTGATCT 850
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 968 AACTCGACTTCCAAACGAAACCTTGGCCCTCTATATCGAGCATTTGCCAAGGACCTAGTAC 1027
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 851 ATAAATGCTCGAAAGSAGCCCAAGAACGCCATTTTCTGCTCATGAGCCCTTGTGTCAAC 910
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1028 GAGGGATGCTAGCCCAAGACCCGAGAGAGCGCTTACTGCTGCCAGGTTCTTGAGCATC 1087
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 911 CATGGATTGCTGATGAACAGACGACCCAGAACGCTCTGTATCCAGAGAGTCTTATCTC 970
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1088 CATGGATGCCAGAGATGGAGAGCATCTGCACAGACCACCTAGATAGCGCTGTTCTCTCAA 1147
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 971 GTCTTAAGCAGTTTCTCAATCAATGAATTAAGAAATGGAATGACGGTAAATTCGCTG 1030
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1148 GAATGAAGCAATTCAGAGCAATGAACAACTCAAGAACTTGGCCCTGAAGTTTATTCGAG 1207
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1031 AGAGACTTTTCAGAGAAAGAAATGGAGCTCTGAAGGAATTTGTTCAAGATGATACACACAG 1090
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1208 AAAATCTCTCAGAGASAAATTCATGAGTGAAGCAATGTTCCAGAAATTCGACACTG 1267
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1091 ACAACAGGCAAGATTACTTTTGAAGAGCTCAAGCGGGTTTGAAGAGAGTGGATCTG 1150
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1268 ACAACAGTGGTACATTTACATACGAAGAACTGAAGAGGGGATTGGCCCACTCGGGGCAA 1327
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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RESULT 11

ABA91081

ID ABA91081 standard; cdNA; 2230 BP.

XX ABA91081;

XX 22-FEB-2002 (first entry)

XX Physcomitrella patens CPK-2 full-length cdNA, SEQ ID NO:26.

XX Protein kinase stress-related protein; PKSRP; moss; protein kinase-6;
XX PK-6; protein kinase-7; PK-7; protein kinase-8; PK-8; protein kinase-9;
XX PK-9; casein kinase homologue-1; CK-1; casein kinase homologue-2; CK-2;
XX casein kinase homologue-3; CK-3; mitogen-activated protein kinase;
XX MAP kinase-2; MPK-2; MAP kinase-3; MPK-3; MAP kinase-4; MPK-4;
XX MAP kinase-5; MPK-5; calcium-dependent protein kinase-1; CPK-1;
XX calcium-dependent protein kinase-2; CPK-2; overexpression;
XX environmental stress; salinity; drought; temperature; tolerance;
XX transgenic plant; EST; expressed sequence tag; ss.

XX Physcomitrella patens.

XX WO200177356-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-US11435.

XX 07-APR-2000; 2000US-196001P.

XX (BADI) BASF PLANT SCI GMBH.

XX Da Costa Silva EO, Bohnert HJ, Van Thielien N, Chen R;

XX Sarria-Millan R;

XX WPI; 2002-049153/06.

XX P-PSDB; AAM52842.

XX New protein, useful for increasing tolerance to environmental stress,
XX comprises a Protein Kinase Stress-Related Protein selected from
XX Protein kinases, Casein Kinase homologs, MAP kinases or Calcium
XX dependent protein kinases

XX Claim 14; Fig 2M; 154pp; English.

XX Sequences AAM52830-AAM52842 represent novel protein kinase stress-related
XX proteins (PKSRPs) from the moss Physcomitrella patens, and sequences
XX ABA91069-ABA91081 represent full-length cDNAs encoding them. The cDNA

sequences were obtained from expressed sequence tags (ESTs: AB91056-AB91068) derived from Physcomitrella patens cDNA libraries. The PKSRPs of the invention comprise protein kinase-6 (PK-6), protein kinase-7 (PK-7), protein kinase-8 (PK-8), protein kinase-9 (PK-9), casein kinase homologue-1 (CK-1), casein kinase homologue-2 (CK-2), casein kinase homologue-3 (CK-3), mitogen-activated protein (MAP) kinase-2 (MPK-2), MAP kinase-3 (MPK-3), MAP kinase-4 (MPK-4), MAP kinase-5 (MPK-5), calcium-dependent protein kinase-1 (CPK-1), and calcium-dependent protein kinase-2 (CPK-2). When overexpressed, the PKSRPs are able to confer tolerance to environmental stresses such as salinity, drought, temperature, metal, chemical, pathogenic and oxidative stress. Physcomitrella patens PKSRP nucleic acids may be used to generate transgenic plants and seeds with increased tolerance to salinity, drought and temperature. The transgenic plants generated can be monocots or dicots and are especially maize, wheat, rice, oat, triticale, rice, barley, cotton, rapeseed, cassava, sunflower, tagetes, leguminous plants (e.g., soybean, peanut, alfalfa), solanaceous plants (e.g., potato, tobacco, aubergine, pepper, tomato), coffee, cacao, tea, Salix species, oil palm, coconut, perennial grasses and forage crops. The PKSRP nucleotide and proteins may also be used in evolutionary and protein structural studies and as markers for specific regions of the genome.

Query Match 30.4%; Score 531.8; DB 24; Length 2230;

Best Local Similarity 62.5%; Pred. No. 1.2e-110;

Matches 849; Conservative 0; Mismatches 507; Indels 3; Gaps 1;

141 TTACCTTCGGGAAAAAGCTAGCCCAAGCCCAATTTGGACACACCTATCTTCGCACAGA 200
 602 TTACATCTCGGGAGGAGCTTCGGAGGGCAGTTCGGAGTCACTTACTTGTGTACTGA 661
 201 GAAATCAACCTCCGCTAAATACGCTGCAAAATCGATCCGCAAGCAAGCTCGTGTGTCG 260
 662 CAGATGACGAATGAGCGCTACGCTGCAAGACATCGCCAAACGGAACAGTACCAGTAA 721
 261 CGAGGATGACGAGATGATGGCGTGAGATTCAGATCATCATCTCTCTGAGCATCC 320
 722 GGAGGATATCGAGGATGTTAAGCGGGAGGTTTCAGATTATCATCATCCTGTCGGGGACCC 781
 321 AAATGTTGTTAGGATCAAGGGACTTAAGAGATTGCGTGTGTTGTTTCATATTTGATGGA 380
 782 CATACTGCTGTTAAAGGATGTTTCGAGGACAGCATTCGTCGATCTTGTGATGGA 841
 381 GGTTCGTGAAGTGGTGGAGCTTTTTCGATCGGATTTTTCATAAGGTCATTTTATGAGCG 440
 842 GCTCTGTGAGTGGGAGCTCTTCGATCATCATTCATTCGCAAGGGGCAATACAGTGAAG 901
 441 TGAAGCTGTCAAGCTTATTAAGAGCATCTTGGTGTGTTGAGCTTGTCTCTCTTGG 500
 902 CGCCGCTGCGGATGTCGAGATCTATGTCATGTCGTCATGTCGATGTCGACATGTCATTAGG 961
 501 TGTTCATGATGATGATCTCAAACTGAGATTTCTTTGATAGTCTCTAAAGATGATGC 560
 962 GATCTTCATCGGATCTCAAGCAGAGATTTCTGTCGCCAGCAAGCTGAGATGC 1021
 561 TAGCTTAAGGCTACCGATTTTGGTTGCTGCTCTCTATTAAGCCAGGACAAATTTATA 620
 1022 GCCTCTGAAGGCCACAGACTTCGCTGTCAACTTTCTTTAAGCCAGGAGATGTGTCCA 1081
 621 TGAGGTAGTTGGAAGTCGCTGATGTCACAGAGGTCCTAAAGAAATGTTATGAGCC 680
 1082 GGATTTGTTGGAAGTCGCTGATGTCGTCGCTGTCGTCGTCGTCGTCGTCGTCGTCGTC 1141
 681 TGAATATGATGTTGGAGTGTGCTGTTGTTATCTCTCTATCTTACTACGCGTGTCTCTCC 740
 1142 TGAAGCTGATGTTGGAGTGCAGCGGTGATGTCATCTCTGCTGTGTGTATACCCCC 1201
 741 CTCTGGGAGAGACTGAGTCTGGAATCTTTAGACAGATATTCGAGGGAGTTAGATTT 800
 1202 CTCTGGGCTGAAACTGAGCAGGGTATCTTTGAGCTGTGTCGTCGTCGTCGTCGTCGTCGTC 1261

801 CAAATCTGACCGTGGCTACTATCTCAGAGCTGCTAAAGATTTGATCTATATAAATGCT 860
 1262 CGAAGCATCCATGCGCGGAAATCTCCACGCGGCTTAGAATTTGTTGAGGAAATGCT 1321
 861 CGAAGGAGCCCAAGAAAGCGCTTTCTGCTCATGAAGCCTTGTGTACCCATGAGTGT 920
 1322 AAACCCCTAAGCTGAAGATAGCTGACGGCACAGCAGGTGTTGAACCATCCATCGATGAA 1381
 921 CGATGACACAGCAGCACCAGACAGCCTTTGATCAGCAGTCTTATCTCTGTTAAAGCA 980
 1382 GGAAGATGTTGATGCTCCAGAGCTGCCACTCGACAATGCGGTGTTGACAGATGAAAA 1441
 981 GTTTCTCAATCAATTAAGATTAAGAAATGCGATACGGGTAAATGCTGAGAGATTTTC 1040
 1442 TTTCTCAGCCGCAACAAGATGAAGAAGTGGCGCTCAAGGTGATTCGACAGATCTGTC 1501
 1041 AGAGGAAGAATTTGAGGTCTGAAGAAATTTTCAAGATGATAGACACAGACAGACGG 1100
 1502 GGAGGAAGATGCTGGGTGAGGGAGATTTTCAATCCATAGATACAGACAGACGG 1561
 1101 AACGATTACTTTGAAGAGCTCAAGCGGTTTGAAGAGAGTCTGATCTGAATGATGGA 1160
 1562 CACGGTACCTCGAGGAGCTTAAGGAAGGTTGCTGAAGCAGGGCTCAAAACTTTAATGA 1521
 1161 ATCAGAAATCAAGTCTCTCATGATCGGCTGATATCGACAACAGTGGTACAATAGACTA 1220
 1622 ATCGGATCAGGAAACTAATGAAGCTGCAGATGTCGATGGAACGCGCAAGATCGACTT 1681
 1221 CGGAGATCTCTAGCAGACCTTACACATGAACAAGATGAGAGAGAGAGATTTCTGGT 1280
 1682 CAACGAGTTCATATCGGCAACTGACATGAACAAGACGGAAGAGAGATCACCTTTG 1741
 1281 GGTGATTTTCGAGCTTTGACAAAGACGGAAGCGTATATCACCATGATGAGCTTCA 1340
 1742 GGAGATTCATCATTCATTCGACAGGACATACGGGTATATCACCATCGACGAGCTCA 1801
 1341 GTCAGCTTCGACAGATTTGGTCTATGTATAC---ACCTCTGGACAGATGATCAAGGA 1397
 1802 GGAAGCAATGGAGAAGATGGAATGGAGATCTGAGACCATCCAGAGATCATCAGCGA 1861
 1398 GATTGATCTTGACATGACGGGAAGATCGATTTCTCGAGTTTACAGCAATGATGAGAA 1457
 1862 GTTGGACACAGACACGACGGAAGATAGACTACGAGGAGTTCGTAGCCATGATGCGCA 1921
 1458 AGGAGATGAGTTGGGAGAGCAGAACCATGATGAAGAA 1496
 1922 GGGCAATCCTGGCGCTGAAAACGGAGGAAGCGTGAACAA 1960

RESULT 12

AAF74281
 ID AAF74281 standard; DNA; 1647 BP.

XX AAF74281;

XX AAF74281;

DT 04-MAY-2001 (first entry)

XX Liverwort calcium dependent protein kinase clone #1.

DE Calcium dependent protein kinase; CDPK; herbicide resistance;

KW paraquat; diquat; crop production; ds.

XX Marchantia polymorpha.

OS WO200107592-A2.

PN 01-FEB-2001.

XX 26-JUL-2000; 2000WO-GB02876.

PF 27-JUL-1999; 99GB-0017642.

XX (ZENE) ZENECA LTD.

XX PI Holt CD, White AJ, Michael AJ, Osborn RW;
 XX DR WPI; 2001-168549/17.
 XX PT Producing herbicide resistance plants by inhibiting calcium dependent
 PT protein kinase in plants or by providing an intracellular vacuolar
 PT transporter capable of transporting agrochemical into plant vacuole
 XX
 XX PS Claim 18; Page 42; 50pp; English.
 XX CC The present invention describes a method of producing plants which are
 CC resistant to the herbicides paraquat and diquat, involving inhibiting in
 CC the plants a calcium dependent protein kinase (CDPK) and selecting those
 CC plants which are resistant to the agrochemical of interest. This is
 CC useful in the production of crops with herbicide resistance.
 XX
 XX SQ Sequence 1647 BP; 447 A; 349 C; 465 G; 386 T; 0 other;
 Query Match 29.9%; Score 523; DB 22; Length 1647;
 Best Local Similarity 62.7%; Pred. No. 1.1e-108;
 Matches 830; Conservative 0; Mismatches 490; Indels 3; Gaps 1;
 QY 141 TTACTTCTGGAAAAAGCTAGGCCAAGCCCAATTTCGAAACACCTATCTCTGCACAGA 200
 DB 240 TTACACCTCGGACGGGAACCTGGCTGGTTCAGTTTGGTGTACGCAATTGTGTACGCA 299
 QY 201 GAAATCAACCTCCGCTAATTAGCCCTGCAAAATCGATCCGGAAGCGAAAGCTCGTGTGCG 260
 DB 300 CAAGGTTACAGTGAGCTTTAGCCCTGCAAGTCAATTCCGAAGAGAGAGTTGACCAATAA 359
 QY 261 CGAGGATTACGAAGAATGATGGCGTGAGATTGAGATCATCATCTCTCTGAGCATCC 320
 DB 360 GGATCAGCTAGAGGATGTTGGGAGGGAAGTCAGATCATGCACCACTTAGAGGGGCGAA 419
 QY 321 AAATGTTGTAGGATCAAGGGACTATCAAGATTCGGTGTGTTGTTATGTTATGGA 380
 DB 420 GAACATTTGCGAATTTGAAGGGGCGCTATGAGGATTAACACAAACAGTCTGTCATGGA 479
 QY 381 GGTGTGTGAAGGTGTGAGCTTTTGTATCGGATTTTCTAAAGGTCAATTTTGTAGTGGG 440
 DB 480 GCTTTGTGCTGCGGAGACCTTCGNCGCCATTTATCAGCGGGCCCATCAGTGTAGAG 539
 QY 441 TGAAGCTGTCAAGCTTATTAAGACGATCTTGGTGTGTTGAGGCTGTGTCATCTCTTGG 500
 DB 540 GSGTGTGTCAGCTCTATGTAGAACTATAGTCAAGTGTTCAGAGCTGCGCATCTCTTGG 599
 QY 501 TGTATGATACAGATCTCAACCTGAGAAATTCCTGTTGATAGTCTCTAAAGATGATGC 560
 DB 600 AGTTATGACCGGGATCTGAAGCCGGAATTTCTGCTGTCTACAGAAAGGAGATGC 659
 QY 561 TAAGCTTAAGGCTACCGAATTTGGTTGCTCTCTCTATAAGCCAGGACAATATTATA 620
 DB 660 ACCCTGAGGCGACGGAATTTGGTCTTCTGCTCTCTCAAGCTTGGAGAGTGTTCAC 719
 QY 621 TGAGTGTGGAAGTCCGCTACTATGTTCCACACAGAGTGCTTAAGAAATGTTATGGACC 680
 DB 720 AGATATCGTGTGAAGTGTCTACTAGTGGCACACAGAGTTTTCGCTGCTAACTATGGGC 779
 QY 681 TGAATATAGATGTGTGAGTGTGTTGTTATCTCTCTACATTTTACTCAGCGGTCTCTCC 740
 DB 780 AGAGGCTGATGTTGTGAGTGTGCGGAGTCAATCTTTACATTTCTTTGTGCGGAGTCCCTC 839
 QY 741 CTCTGGGACAGACTGAGTCTGGAATCTTTAGACAGATATTGCAAGGGAAGTTAGATT 800
 DB 840 TTCTGGGACAGACCGACACAGGATTTTGTATGCCGTAATGCAGGTCATATTGATT 899
 QY 801 CAAATCTGACCGCTGSCCTACTATCTCAGAGCTGCTAAAGATTTGATCTATAAATGCT 860
 DB 900 CACTAGTGTCTTGGCTTCAATTTCTCAAAAGGCGAAAGATCTGTTAAAGAGGATGCT 959
 QY 861 CGAAAGGAGCCCAAGAAACGCAATTTCTGCTCATGAGCCCTTGTGTCACCCATGGATTGT 920

DB 960 CAAACAGAACCCAAAGGAGGAGGATTGACGGCCCATGAAAGTTTAAAGTCACCCATGGATTAG 1019
 QY 921 CGATGAACAAGCAGCAGCAGCAAGCCCTCTGTATCCAGCAGCTWTATCTCTCTAAAGCA 980
 DB 1020 TGTTCGGGAGAGCAGCAGCAAAACCACTTGACAACACCGCTGTGTCTAGATTGAAGCA 1079
 QY 981 GTTTTCTCAAAATGAATAGATTAGAAATAGGCAATAGCGGTAAATGCTGAGAGACTTTC 1040
 DB 1080 ATTCACCGCTATGAACAGCTCAAGAACTTGTCTGAAGGTTATCGCAGAGAGTCTTC 1139
 QY 1041 AGAGGAAGAAATTCGAGTCTGAAGGAATTTCTCAAGATGATACACACACACAGCGG 1100
 DB 1140 TGAAGAGAGATCATGGGATTGAAGGAGATGTTTGAAGGTATGACACACACACAGTGG 1199
 QY 1101 AACGATTACTTTTGAAGAGCTCAAGCGGGTTTGAAGAGAGTCCGATCTGAACTGATGGA 1160
 DB 1200 TACAATCACGTTTCGAGGAGTTGAAGGATGCTCTTCAAAAGCAGGAGTCAAAACCTGGCAGA 1259
 QY 1161 ATCAGAAATCAAGTCTCTCATGGATCGGCTGATATCCACACAGTGGTACAAATAGACTA 1220
 DB 1260 GTCAGAAAGTGGCGCAGCTTAATGGCAGCTGCTGATGTGATGGAAATGGCACTATTGACTA 1319
 QY 1221 CGGAAATTCCTAGCAGCAACCTTACACATGAACAAGATGGAGAGAGAGATTCCTGGT 1280
 DB 1320 CTGAGGATTCATACCGCAACCATGCACTTGAATGAATAGAGAGGAGATCATCTTTA 1379
 QY 1281 GGCTGCAATTTTCGGACTTTTGACAAAGCGAAGCGGTTATATFACCATCTGATGACCTTCA 1340
 DB 1380 CGCTCCCTTTCAGCATTTTGTATGAGCAGCAGCAGTGGTTCATCACCATGGAAGAGCTTGA 1439
 QY 1341 GTCAGCTTGCACAGAGTTTGGTCTATGTGATAC---ACTCTGGACGACATGATCAAGGA 1397
 DB 1440 ACAGGCTTTAATTAAGCAGCGGATGGGAGATCCTGATCTCTGAAAGAAATTAATTAGGA 1499
 QY 1398 GATTGATCTTGACAATGACGGGAAGATCGATTTCGGAGTTTACAGCAATGATCAGGAA 1457
 DB 1500 GGTTCACACTGATCATGATGGACGATCACTACACGAGTTCGTTGCCATGATCGTAA 1559
 QY 1458 AGG 1460
 DB 1560 AGG 1562
 RESULT 13
 AAF74270
 ID AAF74270 standard; DNA; 1791 BP.
 XX
 AC AAF74270;
 XX
 DT 04-MAY-2001 (first entry)
 XX
 DE Carrot calcium dependent protein kinase clone.
 XX
 KW Calcium dependent protein kinase; CDPK; herbicide resistance;
 KW paraquat; diquat; crop production; ds.
 XX
 OS Daucus carota.
 XX
 PN WO200107592-A2.
 XX
 PD 01-FEB-2001.
 XX
 PF 26-JUL-2000; 2000WO-GB02876.
 XX
 PR 27-JUL-1999; 99GB-0017642.
 XX
 PA (ZENE) ZENECA LTD.
 XX
 PI Holt CD, White AJ, Michael AJ, Osborn RW;
 XX
 DR WPI; 2001-168549/17.
 XX
 PT Producing herbicide resistance plants by inhibiting calcium dependent

XX Claim 18; Page 43-44; 50pp; English.
 XX The present invention describes a method of producing plants which are
 CC resistant to the herbicides paraquat and diquat, involving inhibiting in
 CC the plants a calcium dependent protein kinase (CDPK) and selecting those
 CC plants which are resistant to the agrochemical of interest. This is
 CC useful in the production of crops with herbicide resistance.
 XX
 XX Sequence 2363 BP; 718 A; 435 C; 542 G; 568 T; 0 other;

Query Match 29.9%; Score 521.6; DB 22; Length 2363;
 Best Local Similarity 60.3%; Pred. No. 2.5e-108;
 Matches 898; Conservative 0; Mismatches 584; Indels 6; Gaps 2;

QY 74 CGAAGCCAAACCTAGAGTCTTCAACACAGTCTTACCATATCAAAACACACGATTA 133
 DB 523 CAAGACCAAGCCCAAGTGTAGCCCAATATCAATTTGGGTAAACCCCTTGGAGTGTGA 582
 QY 134 GAGATCATTAACCTTCTGGGAAAAGCTAGGCCAAGGCCAATTTGGACACACCTATCTCT 193
 DB 583 AGGTGATACATTTGGGAGAGAACCTGGGTAGGGTCAATTTGGGTAAACCCCTTGGAGTGTGA 582
 QY 194 GCACAGAGAAATCAACCTCCGCTTAATAGCGCTGCAAAATCGATCCCGAAGGAAAAGCTCG 253
 DB 643 GCACGTGACAAAAGACTGGCCCAACATATGCTTGCAGCTCAATCTCTAAGAGAAGCTTG 702
 QY 254 TGTGTGGGAGGATTAACGAATGATATGGCGTGAGATTCAGATCATGATCATCTCTCTG 313
 DB 703 TGACCAAGCGGTGAAGATGATATGAGGAGAGATTCAGATCATGAGCATATGAGTG 762
 QY 314 AGCATCCAAATGTTGTAGGATCAAGGAGCTTATGAAGATTCGGTGTGTCATATTT 373
 DB 763 GTCACCTTAACATGTGAATTTAAGGTGCTTATGAGATTAACATCTGTGATCTTG 822
 QY 374 TTATGGAGTTTGAAGTGGTGGAGCTTTTGTATCGGATTTCTTAAAGGTCAATTTTA 433
 DB 823 TGATGGAGCTTTGTGCTGGTGGGAGTGTGTTGATGAGTATTTGCTAAGGGCATTATA 882
 QY 434 GTGAGCGTGAAGCTGCAAGCTTATTAAGACGATTCCTGTTGTTGAGCGCTGTCTATT 493
 DB 883 GTGAAGGCTGTCGCACTATGTGAGGAGATTTGTTGATGAGTATTTGTTGATGCTACT 942
 QY 494 CTCTTGTGTTATGATAGATCTCAAACTGAGATTTCTTGTGATGATGCTTAAAG 553
 DB 943 TTATGGGTGATGATAGGATCTGAGCTGAGACTCTTGTCTCTAGCAAGGATG 1002
 QY 554 ATGATGCTAAGCTTACCGATTTGCTGTTGCTGCTCTTCTATTAAGCCAGGACAAAT 613
 DB 1003 AGAATCTCTCTGAAGGCCACTGATTTGGGTGCTGCTGTTTATTAAGAAAGTAAAG 1062
 QY 614 ATTTATATGAGTGTGGAAGTCCGCTACTATGTTGACAGAGGCTGCTAAGAAATGTT 673
 DB 1063 TCTACCGGATATAGTAGGAGTCTTACTATGTCGCTCTGAGGATTTGCGTCTAGGT 1122
 QY 674 ATGAGCTGAATAGATGTGTGGAGTGTGTTGTTATCTCTACATTTTACTCAGCGGTG 733
 DB 1123 ATGGAAGGAGATGATTTGGAGTGTGAGGATGCTGAGTCTGATCTTACTCTAGTGGTG 1182
 QY 734 TTCTCCCTTCTGGGAGAGACTGAGTCTGGAATCTTTAGACAGATATTTGAAGGGAAGT 793
 DB 1183 TGCCCCCTTTTGGCGAAGACGGAAGGAGGATCTTGTGATCTTATTTGAAGGCCATA 1242
 QY 794 TAGATTTCAATCTGACCCGTGGCTACTATCTCAGAGCTGCTAAGAGATTTGATCTATA 853
 DB 1243 TTGATTTGGAAGCAACACTGGCCATCAATTTCAATGTTGCCAAGGACCTAGTGAGAA 1302
 QY 854 AATGCTGGAAGAGGCCCAAGAAAGCAATTTCTGCTCATGAAAGCTTTGTCCACCAT 913
 DB 1303 AATGTTGACACAGGATCCCAAGAAAGGATTTACTGCTGCTCAAGTTCTTGAGCACCAT 1362
 QY 914 GGATTTGCGATGACACAGCACCACAGACGCTTTGATCCAGAGCTTATCTCTGTC 973

DB 1363 GGCTAAGAGATGGTGAAGCAT---CAGACAAGCCCAATAGACAGTGTCTTCTCTCAGGA 1419
 QY 974 TAAAGCAGTTTTCTCAAAATGAATAAGATTAAGAAATGSCATTACGGGTAAATTTGCTGAGA 1033
 DB 1420 TGAAGCAATTCAGATGATCAAGCAAGCTCAAGAACTCGCTCTAAGGTCAATTTGCTGAAA 1479
 QY 1034 GACTTTCAGAGAAAGAAATTTGGAGTCTGAAGGAATTTGTTCAAGATGATAGACACAGCA 1093
 DB 1480 ATCTTTCTCTGATGAAGAGATCCAAAGGCTGAAACAAATGTTCCGAATATGGCACTGATG 1539
 QY 1094 ACAGCGGAAGGATTAATTTTGAAGAGCTCAAGCGGGTTTGAAGAGATCGCATCTGAC 1153
 DB 1540 GTAGTGGGTCAATTAACCTATGAAGAACTGAGGAGGGGATTTGGCTCGACTTGGATCAAGC 1599
 QY 1154 TGATGGAATCAAGAAATCAAGTCTCTCATGGATGCGGCTGATATCGACAACAGTGTGACAA 1213
 DB 1600 TTACTGAAACTGAAGTGAAGGCGCTCATGGAAGCTGCTGATCAAGATGGAAGTGGATCAA 1659
 QY 1214 TAGACTAGGAGAAATTCCTAGCAGCAACCTTACATGAACAAAGATGGAGAGAGAGAGA 1273
 DB 1660 TAGACTATGATGATTTACAGCCCAATGATAGGTACAGGTTCAGAGAGATGAGC 1719
 QY 1274 TTCGCTGCTGCTGCTTTTCGGACTTTGACAAAGCGGAGCGGTTATATCACCATCGATG 1333
 DB 1720 ATCTTTCAAGCATTCOAATATTTTCGACAAGCAATAGTGGGTTTATCAACACAGATG 1779
 QY 1334 AGCTTCACTGCTTGCACAGAGTTTGGTCTATGTGAT---ACACCTCTGGACGACATGA 1390
 DB 1780 AACTAGAAACAGCAATGAAGATGATGGATTCGTGATGAGAAATTCGATTCAGAGATAT 1839
 QY 1391 TCAGGAGATTTGATCTTGCATATGACGGGAAGATGCGATTTCTCGGAGTTTACAGCAATGA 1450
 DB 1840 TGTGGAAGTACACACTGATATGATGAAGAAATAAATATGATGATGATGATGATGATGATG 1899
 QY 1451 TGAGGAAAGGAGATGGAGTTGGGAGAGCAGAACCATGATGAAGAACTTGAACCTCAACA 1510
 DB 1900 TGAGAGTGGGACTCAAAACCGGTTTACCAACTCATTTAGTGGATGTCATTTCTTACGA 1558
 QY 1511 TTGCTGATGCTTTTGGAGTTGATGTTGAAATCTGATGACTGACTCA 1558
 DB 1960 CTGTATAACGTAAAGCGCTTTTAAAGTACCAAGGTTATGAACAGTCA 2007

RESULT 15
 AAF74273
 ID AAF74273 standard; DNA; 2436 BP.
 XX AAF74273;
 AC
 XX
 XX
 DT 04-MAY-2001 (first entry)
 XX
 DE Soybean calcium dependent protein kinase clone #1.
 XX
 XX Calcium dependent protein kinase; CDPK; herbicide resistance;
 KW paraquat; diquat; crop production; ds.
 XX
 OS Glycine max.
 XX
 PN WO200107592-A2.
 XX
 XX 01-FEB-2001.
 XX
 XX 26-JUL-2000; 2000WO-GB02876.
 XX
 XX 27-JUL-1999; 99GB-0017642.
 XX
 XX (ZENE) ZENECA LTD.
 PA Holt CD, White AJ, Michael AJ, Osborn RW;
 XX WPI; 2001-168549/17.
 DR
 XX Producing herbicide resistance plants by inhibiting calcium dependent

PT protein kinase in plants or by providing an intracellular vacuolar
PT transporter capable of transporting agrochemical into plant vacuole
XX
FS Claim 18; Page 36-37; 50pp; English.

XX The present invention describes a method of producing plants which are
CC resistant to the herbicides paraquat and diquat, involving inhibiting in
CC the plants a calcium dependent protein kinase (CDPK) and selecting those
CC plants which are resistant to the agrochemical of interest. This is
CC useful in the production of crops with herbicide resistance.

XX Sequence 2436 BP; 738 A; 435 C; 515 G; 747 T; 1 other;

Query Match 29.8%; Score 520.2; DB 22; Length 2436;
Best Local Similarity 64.5%; Pred. No. 5.2e-108;
Matches 793; Conservative 0; Mismatches 433; Indels 3; Gaps 1;

QY 143 ACCCTTCGGGAAAAGCTAGGCCAAGCCAAATTGGAACAACCTATCTCTGCACAGAGA 202
DB 739 ACACACTGGGAAGAGTTGGGTAGAGGGCAATTTGGTGTGCACATATCTTTGCACAG 798
QY 203 AATCAACTCCGCTAATACCCCTGCAATCGATCCCGAAGCGAAGCTCGTGTGTCGG 262
DB 799 ATTGACCGGATTCGAGTATCCCTGCAAGTCCATTTCCAGAGGAAACTTCCGAGCAAA 858
QY 263 AGGATTACGAAGATGTATGGCGTGAGATTCAGATCATGCTCTCTCGAGCATCAA 322
DB 859 CTGATAGGAGGACATGAAGAGGAGATTCAGATTATGCACATTTGAGTGGTCAACCCA 918
QY 323 ATGTTGTAGGATCAAGAGGACTTATGAAGATCGGTGTTTGTTCATATTTATGAGGAG 382
DB 919 ACATTGTGTAGTTCAAGAGGCTTATCAGGATAGAGCTCAGTTTCATCTTGTGATGGAG 978
QY 383 TTTGTGAAGTGGTACGCTTTTCATCGGATGTTTCTAAAGGTCAATTTAGTGAAGCGTG 442
DB 979 TGTGTGAGGTGGGAACTTTTGTATAGGATTTGTCCAGAGGGGCATTCAGTGAAGG 1038
QY 443 AAGCTGTCAAGCTTATTAAGACGATTTCTTGGTGTGTTGTAGGCTTGTCATCTCTTGGTG 502
DB 1039 CTGCTGCTTCAATTTGCAGACAAATTTGAATGTTGTTCATATCTGTCTATTTTCATGGTG 1098
QY 503 TTATGCTATAGAGATCTCAACCTCAGAAATTTCTTGTGTATGATGCTTAAAGATGATGCTA 562
DB 1099 TGATGCTATAGGATCTGAACACAGAAATTTTGTCTATCTAGTAGGAGCAGCAAAATGCAC 1158
QY 563 AGCTTAAGGCTACCGATTTTGGTGTGCTGCTTCTATAGCCAGGACAAATTTATATG 622
DB 1159 TTCTCAAGGCAACGATTTTGGCTTGTGCTGTTTCATTTGAAGAGGAAAGGTATATCGGG 1218
QY 623 ACGTAGTGAAGTCCGTACTATGTTGCACAGAGTGTCTAAAGAAATGTTATGAGCTG 682
DB 1219 ATATAGTGTGTAGTGTCTACTATGTTCTCTGAAGTCTCGCGCGCAGATGTGGGAAG 1278
QY 683 AAATAGATGTGTGAGTGTGTTTATCCTCTACATTTTACTCAGCGGTGTTCCCTCCCT 742
DB 1279 AAATAGATATATGAGTGTGAGGATCATATTTATATCTTACTTGTAGTGGAGTCCCTCCAT 1338
QY 743 TCTGGGCGAGACTGAGTCTGGAATCTTTAGACAGATATTCGAAGGAAAGTTAGATTTCA 802
DB 1339 TTTGGGCTGAGACTGAGAAGGAATATTTGATGCCATATTTGAAGGTCACATTTGATTTTG 1398
QY 803 AATCTGACCCGTGCCCTACTATCTCAGAAGCTGTAAAGATTTGATCTATAAAATGCTCG 862
DB 1399 AAAGTCAACCATGCTTAACATCTCAGACAGTCCAGGATCTTGTTCGTAAGATGCTTA 1458
QY 863 AAAGAGCCCCAAGAACGCAATTTCTGCTATGAAGCTTGTGTCAACCATGGAATGTGCG 922
DB 1459 TACAGGATCCAAAGAAAGCAATTAACCTCTGCTCAAGTCTTGTAGCACCACCATGGAATTAAG 1518
QY 923 ATGAACAGCAGCAGCAGCAGGCTCTTGTATCCAGAGTCTTATCTGCTCTAAGCAGT 982
DB 1519 ATGGAAA---TGCTTCAGACAAAGCCGATAGACAGTGCAGTCTCTTCCAGATGAAGCAAT 1575

QY 983 TTTCTCAATGAATPAAGATTAAGAAAATGGCATTTACGGTAAATTCCTCAGAGACTTTTCAG 1042
DB 1576 TTAGAGCAATGAATTAAGCTAAAGAAACTTGCCTTTGAAGGTCATTCTCTGAGAAATATGCTG 1635
QY 1043 AGGAAGAAATTTGGAGGCTCTGAAGGAATTTCTCAAGATGATAGACACAGACACAGCGGAA 1102
DB 1636 CAGAGAGATCCCAAGGTTTGAAGCAATGTTTACAATATGGACACTGACAGAGTGGTA 1695
QY 1103 CGATTACTTTTGAAGAGCTCAAGCGGGTTTGAAGAGAGTGGGATCTGAACTGATGAAGT 1162
DB 1696 CAATCACTATGAAGAACTTAAAGTCAGGATTCATAGACTTGGCTCAAGCTTACAGAGG 1755
QY 1163 CAGAAATCAAGTCTCTCATGGATCGGCTGATATCGACACAGTGGTACATAGACTACG 1222
DB 1756 CTGAAGTGAAGCAACTTATGGAAGCTGCTGATGTAGATGGAATGGCTCAATTGACTACA 1815
QY 1223 GAGAAATTCCTAGCAGCAACCTTACACATGACAAAGATGGAGAGAGAGAGATTTCTGGTGG 1282
DB 1816 TAGAATTCATCAGTCTACATGCAATGCAATAGACACAAATTAGAAGAGAGATGACCAACTTTTCA 1875
QY 1283 CTGCATTTTCGGACTTTGACAAAGACGGAAGCGGTTTATATACCATCGATGAGCTTCAGT 1342
DB 1876 AGGCTTTCCAATATTTTGAAGAGACAAACAGTGGGTTTATATACAAGAGATGAATTTGAAT 1935
QY 1343 CAGCTTGCACAGAGTTTGGTCTATGTGAT 1371
DB 1936 CAGCCATCAAGAAATATGGTATGGTGTAT 1964

Search completed: March 26, 2003, 07:52:20
Job time : 527 secs

INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 1349 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 3..1226
OTHER INFORMATION: /note= "cDNA sequence for maize
pollen-specific calcium dependent protein kinase gene as
disclosed in Figure 30."
US-07-951-715A-20

Query Match 24.6%; Score 429.8; DB 1; Length 1349;
Best Local Similarity 60.3%; Pred. No. 1.4e-99;
Matches 729; Conservative 0; Mismatches 477; Indels 3; Gaps 1;

290 TTCAGATCATGATCATCTCTCTGAGCATCCAAATGTTGTAGGATCAAAAGGGAGCTTATG 349
1 TGCAGATCATGACCACTCTCCGGCAGCCACACGTCGTGGGCTCCGGCGCGCTACG 60
350 AAGATTCGGTGTGTTTCATATTGTTATGAGGTTTGTGAAGTGTGTGAGCTTTTGTATC 409
61 AGCACAACAGAGAGCGTGCACCTCTCATGAGCTGTGCGGGCGGGAGCTCTTCGACC 120
410 GGATGTTTCTAAGGTCATTTAGTGTGAGGCTGAGCTGTCAAGCTTATTAGACGATTC 469
121 GCATCATCGCCGGGCGGCTACACGAGCGCGCGCGCGGAGCTCTGCGGCGCCATCG 180
470 TTGGTGTGTTGAGGCTGTCTCTCTGTTGTTATGATAGATCTCAAACTCTGAGA 529
181 TGCAGATCGTGCACACTGCCATCTCATGCGGTGATGACCGGAGCATCAAGCCCGAGA 240
530 ATTCTTCTTATAGCCAGGACATATTTATATGACGTAGTGTGAAGTACCGATTTTGGTTGT 589
241 ACTTCTGTCTCAGCAGAGGAGGAGCGCGCGCTCAAGGCCACCGACTTCGGGCTCT 300
590 CTGCTCTTCTAAGCCAGGACATATTTATATGACGTAGTGTGAAGTACCGATTTTGGTTGT 649
301 CCGTCTCTTCAAGGAGGCGAGCTGTCTAGGACATCTGCGGCGGCTGCGGCTCA 360
650 CACGAGGTCGTAAGAAATGTTATGACCTGAAATAGATGTGTGAGTGTGTTGTTA 709
361 CGCCCGAGGTGCTCAAGAGGAAGTACGGCCGCGGAGCGGACATCTGGAGCTGCGGCTCA 420
710 TCCTCTACATTTACTCAGCGGTGTTCTCCCTCTTGGGCGAGACTGAGTCTGGAATCT 769
421 TGCTCTACATCTTCTCGCGCGGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 480
770 TTAGCAGATATTGCAAGGGAAGTTAGATTTCAAACTGTACCGCTGCGCTACTATCTCAG 829
481 TCACCGGCATCTCTGCGAGGCGACCTTGACCTCTCCAGCGAGCCATGCGCCACATCTCGC 540
830 AAGCTGCTAAGATTTGATCTATAAATGCTCGAAGGAGCCGCCAAGAAACGCAATTTCTG 889
541 CGGAGCCCAAGGATCTCGTCAAGAGATGCTCAACATCAACCCCAAGGAGCGGCTCAGCG 600
890 CTCATGAAGCTGTGTACCCATGATGTCATGAACAGCAGCAGCAGCAGCAGCAGCAGCCTC 949
601 CGTTCAGGCTCTCAATCACCCATGATGATCAAGAGAGGAGGAGGAGGAGGAGGAGGAGG 660
950 TTGATCAGAGCTTTATCTCTCTCAAGCAGTTTCTCAATGAATGAATTAAGAAATAA 1009
661 TTGACAAAGTGTCTCGACAGGCTCAAGAGTTTCCAGGCGCATGACAGGCTCAAGAAAG 720
1010 TGCATTAACGGGTAATGCTGAGAGACTTTCAGAGGAGAAATTTGAGGCTCTGAAGGAAT 1069
721 CAGCATTGAGGATCATGATGCTGGTGTCTATCCGAGAGGAGATCACAGGCTCTGAAGGAG 780
1070 TGTTCAGATGATAGACAGACACAGCGGAGACGATTTTGTGAGAGCTCAAGCGG 1129

781 TGTTCAAGACATTGCAAGGATAACAGCGGACCATTAACCTCGACGAGCTCAACACG 840
1130 GTTTGAAGAGAGTCGGATCTGAATGATGAATCAGAAATCAAGTCTCTCATGTATGGG 1189
841 GGTGGCAAGCAGCGGCCCAAGCTGTACAGACAGCGAATGGAGAACTATATGAAGCAG 900
1190 CTGATATCGACACACAGTGGTACATATAGACTACGAGAAATCTTACAGCAGCACTTACACA 1249
901 CTGACGCTGACGCGACAGCGGTTTATTGACTACGACGAATTCGTCCGCAACAGTGCATA 960
1250 TGAACAAGATGGAGAGAGAGGATTTCTGTGGCTGCAATTTCCGACTTTGACAAAGACG 1309
961 TGAACAACCTGGATAGAGAGAGACCTTTACACAGCATTCCTGATATTCGACAGGACA 1020
1310 GAAGCGGTTATATACCATCGATGAGCTTCAGTCAGCTTCGACAGAGTTTGGTCTATGTG 1369
1021 ACAGCGGTTACATTACTTAAAGAGAGCTTGAGCAGCGCTTGAAGGACCAAGGTTGTATG 1080
1370 ATACACT---CTGAGCAGCATGATCAAGAGATTTGATCTTGACATATGACGGAAGATCG 1426
1081 ACGCCGATAAATCAAGACATCATCTCCGATGCCGACTCTGACATATGATGAAGGATAG 1140
1427 ATTCTCGGAGTTTACAGCAATGATGAGGAAAGAGATGGAGTTGGGAGAGCAGACCA 1486
1141 ATTATTCAGATTTGTGGCATGATGAGGAAAGGAGCGGCTGGTGGCGGACCAATGAACA 1200
1487 TGATGAAGA 1495
1201 TCAAGAAGA 1209

RESULT 2

US-08-459-448A-20
Sequence 20, Application US/08459448A
Patent No. 5859336
GENERAL INFORMATION:
APPLICANT: Kozziel, Michael G.
APPLICANT: Desai, Nalini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merila, Ellis J.
APPLICANT: Launis, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5859336artis Corporation
STREET: Patent & Trademark Dept., 520 White Plains
STREET: Rd., POB 2005
CITY: Tarrytown
STATE: New York
COUNTRY: USA
ZIP: 10591-9005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,448A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 800

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/951,715
 FILING DATE: 25-SEP-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/772,027
 FILING DATE: 04-OCT-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Pace, Gary M.
 REGISTRATION NUMBER: 40403
 REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (919)541-8582
 TELEFAX: (919)541-8689
 INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1349 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 3..1226
 OTHER INFORMATION: /note= "cDNA sequence for maize
 OTHER INFORMATION: pollen-specific calcium dependent protein kinase gene as
 OTHER INFORMATION: disclosed in Figure 30."
 US-08-459-448A-20

Query Match 24.6%; Score 429.8; DB 2; Length 1349;
 Best Local Similarity 60.3%; Pred. No. 1.4e-99;
 Matches 729; Conservative 0; Mismatches 477; Indels 3; Gaps 1;

290 TTCAGATCATCATCTCTCIGAGCATCAAAAGTTGTTAGATCAAAAGGGACTTATG 349
 1 TGCAGATCATCTCCCGGCGAGCCCAACGGTGGTGGGCTCGCGGCGCGTACG 60
 350 AAGATTCGGTGTTCATATTTATGAGAGTTGTTGAGGTGGTGGCTTTTGTATC 409
 61 AGGCAAGCAGACGGCTGACCTCTCATGAGCTGTGCGGGCGGGAGCTCTTCGACC 120
 410 GGATTTGTTTAAAGTCAATTTAGTGAAGCTGAAGCTGCAAGCTTATTAAAGCATTC 469
 121 GCATTCGCGCGGGGCGAGTACACGAGGCGGCGGCGGAGCTGTGCGGCCCATCG 180
 470 TTGCTGTGTGAGGCTGTGATCTCTCTGTTATGATGATGATGATGATGATGATGAT 529
 181 TGCAGATCGTGCACACTGCCACTCCATGGGGGTGATGACCGGGAGATCAAGCCGAGA 240
 530 ATTCTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 589
 241 ACTTCTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
 590 CTGCTCTCTATAGCAGGACATATTTATGACGTAGTGTGAGTGTGAGTGTGAGTGTGAG 649
 301 CCGTCTCTCTTCAAGAGGGGCGAGTGTCTCAGGGACATCGTGGCGAGCGCTACTACATCG 360
 650 CACGAGAGTGTCTAAAGAAATGTTATGAGCTGAAATAGATGTTGAGTGTGAGTGTGAGT 709
 361 CGCCGAGGTGCTCAAGAGGAAGTACCGCGGAGGCGGACATCTGGAGCGTGGCGGTCA 420
 710 TCTCTCTACATTTACTCAGCGGTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 769
 421 TGCTCTACATCTTCT 480
 770 TTAGACAGATATTCCAGAGGAAGTTAGATTTCAATCTGACCGGTGGCTTACTATCTCAG 829
 481 TCACCGGCATCTCTCGAGGGCAGCTTGACCTCTCCAGCGAGCATGCCACACATCTCCG 540
 830 AAGCTGTCTAAGATTTGATCTATAAATGCTCGAAGAGGAGGAGGAGGAGGAGGAGGAGG 889
 541 CGGAGGCAAGGATCTCGTCAAGAAGATGCTCAACATCAACCCCAAGGAGCGGCTCAGG 600

890 CTCATGAAGCCCTTGTCTACCCATGATGTTGTCATGAACAGCAGCAGCAGCAGCAGCCTC 949
 601 COTTCCAGGTCTCTCAATCAACCATGATCAAAAGAGAGCGGAGCGGCTGACACGCCGC 660
 950 TTGATCCAGCAGTCTTATCTGTTAAAGCAGTTTCTCAATGAATGAATGAATGAATGA 1009
 661 TTGACAACGTTGTTCTCGACAGGCTCAAGCAGCTTCAAGGCCATGAACGAGTTCAAGA 720
 1010 TGGCATTACGGGTAAATGCTGAGAGACTTTCAGAGGAAGAATTCGAGGCTCTGAAGGAT 1069
 721 CAGCATTGAGGATCAAGCTGGTCCCTATCCGAAGAGAGATCACAGGCTGGAAGGAGA 780
 1070 TGTTCAGATGATGACACAGACACACGCGGAAGATTACTTTTGAAGAGCTCAAGCGG 1129
 781 TGTTCAAGAACATTGACAAGGATAACAGCGGAGCACCATTACCTCGACGAGCTCAACAC 840
 1130 GTTTCAGAGAGTGGATCTGAACCTGATGAATCAGAATCAAGTCTCTCATGATGCGG 1189
 841 GTTGGCAAGACACGCGGCCCAAGCTGTGACAGAGGAATGGAGAACTAATGGAAGCAG 900
 1190 CTGATATGCAACACAGTGGTACATAGACTACGGAGAATTCCTAGCAGCAACCTTACACA 1249
 901 CTGACGCTGACGGCAACGGGTTAATTGACTAGCAGCAATTCGTCAACCCACAGTGCATA 960
 1250 TGAACAAGATGAGAGAGAGAGATTTGTTGGCTGCTGCTTTTGGACTTTGACAAAGACG 1309
 961 TGAACAACACTGGATAGAGAGAGACACCTTTACACAGCATTCACAGTATTTTCGACAAG 1020
 1310 GAAGCGGTATATCACCATCGATGAGCTTCAGTTCAGCTGTCACAGAGTTTGTCTATGTG 1369
 1021 ACAGCGGTACATTTACTTAAAGAGAGCTTGAGCAGGCTTGAAGAGCAAGGTTGTATG 1080
 1370 ATACACCT---CTGAGCAGATGATCAAGAGATTTGATTTTGAATGACGCGGAGATCG 1426
 1081 ACGCGGATAAAATCAAGACATCATCTCCGATGCCGATCTGCAATGATGGAAGGATAG 1140
 1427 ATTTCTCGAGTTTACAGCAATGATGAGGAAGAGATGAGTGGAGTGGGAGAGAGACCA 1486
 1141 ATTATTCAGAGTTTGTGGGATGATGAGGAAGGAGCGGCTGGTGGCGAGCAATGAACA 1200
 1487 TGATGAAGA 1495
 1201 TCAAGAAGA 1209

RESULT 3
 US-08-459-595A-20
 Sequence 20, Application US/08459595A
 Patent No. 6018104
 GENERAL INFORMATION:
 APPLICANT: Kosziel, Michael G.
 APPLICANT: Desai, Nalini M.
 APPLICANT: Lewis, Kelly S.
 APPLICANT: Kramer, Vance C.
 APPLICANT: Warren, Gregory W.
 APPLICANT: Evola, Stephen V.
 APPLICANT: Crossland, Lyle D.
 APPLICANT: Wright, Martha S.
 APPLICANT: Merlin, Ellis J.
 APPLICANT: Launis, Karen L.
 APPLICANT: Rothstein, Steven J.
 APPLICANT: Bowman, Cindy G.
 APPLICANT: Dawson, John L.
 APPLICANT: Dunder, Erik M.
 APPLICANT: Pace, Gary M.
 APPLICANT: Suttie, Janet L.
 TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
 TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
 NUMBER OF SEQUENCES: 94
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: No. 6018104artis Corporation
 STREET: Patent & Trademark Dept., 520 White Plains
 STREET: Rd., POB 2005

CITY: Tarrytown
STATE: New York
COUNTRY: USA
ZIP: 10591-9005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,595A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: 40403
REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8582
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 1349 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: 3: 1226
LOCATION: 3: 1226
OTHER INFORMATION: /note= "cDNA sequence for maize
OTHER INFORMATION: pollen-specific calcium dependent protein kinase gene as
OTHER INFORMATION: disclosed in Figure 30."
US-08-459-595A-20
Query Match 24.6%; Score 429.8; DB 3; Length 1349;
Best Local Similarity 60.3%; Pred. No. 1.4e-99;
Matches 729; Conservative 0; Mismatches 477; Indels 3; Gaps 1;
QY 290 TTCAGATCATGATCATCTCTGAGCATCCAAATGTTGTAGATCAAAAGGACTATG 349
DB 1 TGCAGATCATGACACACCTCTCGGGCCAGCCCAACGTTGGTGGCCCTCCGGCGCGCTACG 60
QY 350 AAGATTCGGTGTGTTGTCATATTGTTATGAGGTTTGTGAAGTGGTGGAGCTTTTGTATC 409
DB 61 AGGACAAGCAGACGCTGCACCTCGTCAAGGAGTGTGCGGGGGGGAGCTCTTCGACC 120
QY 410 GGATTGTTCTAAAGTTCATTTTGTAGTGGGTGAAGCTGTCAAGCTTATTAAAGCATTC 469
DB 121 GCATCATCGCCGGGGCCAGTACAGCGCGCGCGCGGAGCTGCTGCGCGCCATCG 180
QY 470 TTGGTGTGTGAGGCTTGTGTCATCTTCTGTTATGAGGTTTGTGAAGTGGTGGAGCTTTTGTATC 529
DB 181 TGCAGATCGTGCACACCTGCGACCTCCCATGGGGTGTGATGACCGGGAGCATCAAGCCCGAGA 240
QY 530 ATTCTTGTGTGAGTCCCTAAAGCATGATGCTAAGCTTAAGCTACCGATTTCGTTGTGT 589
DB 241 ACTTCTCTGCTCTCAGCAAGACCGAGGACGCGCGCTCAAGGCCACCGACTTCGGCCCTCT 300
QY 590 CTGCTCTTATAAGCCAGGACATATTATATGACGTAGTTGGAAGTCCGCTACTATGTTG 649
DB 301 CCGTCTTCTCAAGGAGGCGGAGCTGCTCAGGACATGCTGCGGAGCGGCTACTACATCG 360
QY 650 CACGAGAGGTGCTAAAGAAATGTTATGGAACCTGAAATAGATGTGTGGAGTCTGTTGTA 709
DB 361 CGCCCGAGGTGCTCAAGAGGAAGTACGCGCGGAGCGGAGCTCTGGAGCGCTCGGCGTCA 420

RESULT 4
US-08-459-504B-20
; Sequence 20, Application US/08459504B
; Patent No. 6075185
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.

APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6075185artis Corporation
STREET: 3054 Cornwalis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,504B
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/459,595
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Melis, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC1577/CIP/DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 1349 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 3..1226
OTHER INFORMATION: /note= "cDNA sequence for maize
OTHER INFORMATION: pollen-specific calcium dependent protein kinase gene as
OTHER INFORMATION: disclosed in Figure 30."

us-08-459-504B-20

Query Match 24.6%; Score 429.8; DB 3; Length 1349;
Best Local Similarity 60.3%; Pred. No. 1.4e-99;
Matches 729; Conservative 0; Mismatches 477; Indels 3; Gaps 1;
QY 290 TTGAGATATGATATCTCTGAGCATCCAAATGTTGTAGGATCAAGAGGACTTATG 349
DB 1 TGCAGATATGACCACTCTCCGGCCAGCCCAACGTGTGGGCTCCGGCGGCGTACG 60
QY 350 AAGATTCGGTGTGTCATATGTTATGAGGTTTCTGAAGTGTGTGAGCTTTTGTATC 409
DB 61 AGGCAAGCAGACGCGTGCACCTGTGATGAGCTGTGCGGCGGCGGAGCTCTTCGACC 120
QY 410 GGATTTCTTAAAGTTCATTTTAGTGAGCGTCAAGCTGTCAAGCTTATTAAGCAATTC 469
DB 121 GCATATCGCCGGGCCAGTACACGAGCGCGGCGGCGGAGCTGCTCGCGCCATCG 180
QY 470 TTGGTGTGTGAGGCTTGTCTATCTCTTGGTGTATGATAGATCTCAAACCTGAGA 529

DB 181 TGCAGATCGTGACACACTGCCACTCCATGGGGTGTATGACCGGGACATCAAGCCGAGA 240
QY 530 ATTTCTTTGTTTATAGTCCCTAAAGATGATGCTAAGGCTTAAGGCTTACCGATTTGTTGT 589
DB 241 ACTTCTTGTCTCAGCAAGACAGGACGCGCTCAAGGCCACCGACTTCGGCCCTCT 300
QY 590 CTGCTTCTTATAAGCCAGGACAATATTATATGACGTAGTTGGAAGTCCCTACTATGTTG 649
DB 301 CCGTCTTTCTCAAGGAGGCGAGCTGCTCAGGGACATCGTCCGCGAGCGCTACTACATCG 360
QY 650 CACCAGAGTGTCTAAAGAAATGTTATGAGCTGAAATAGATGTGTGAGTGTGTTGTTA 709
DB 361 CGCCGAGGTGCTCAAGAGGAAGTACGCGCCGGAGCGCATCTGGAGGTGCGCGTCA 420
QY 710 TCCTCTACATTTTACTCAGCGGTGTTCTCCCTTCTGGGAGAGACTGAGTCTGGAATCT 769
DB 421 TGCTCTACATCTTCTCGCGCGGTGCTCTCTTCTGGGAGAGACGAAACGGCACT 480
QY 770 TTAGACAGATTTGCAAGGAAGTTAGATTTCAAATCTGACCCCTGCTCTACTCTCAG 829
DB 481 TCACCGGCATCTCGGAGGCGAGCTTCACCTCTCCAGGAGCCATGCCACATCTCGC 540
QY 830 AAGCTGCTAAGATTTCATCTATAAATGCTCGAAGGAGCCCCCAAGAACGCACTTCTG 889
DB 541 CGGAGGCCAAGGATCTCGTCAAGAAGATGCTCAACATCAACCCCAAGGAGCGCTCAC 600
QY 890 CTCATGAAGCCTTGTGTACCCATGGATTCTCGATGAACAAGCAGCAGCAGCAAGCGCTC 949
DB 601 CGTTCCAGGTCTCAATCACCCATGGATCAAGAAGACGGAGAGCGCCCTGACACGCGC 660
QY 950 TTGATCCAGCAGCTTATCTGCTTAAAGCAGTTTCTCAATGAATPAAGATTAAAGAAA 1009
DB 661 TTGACAACGTTGTTCTCGACAGGCTCAAGCAGTTTCAGGGCCATGAACCACTTCAAGA 720
QY 1010 TGCATTACGGTAAATGCTGAGAGACTTTCAGAGGAGAANTTGGAGGTCTGAAGAAAT 1069
DB 721 CAGCATTTGAGGATCATAGCTGGGTGGCTATCCGAAGAGGAGATCACAGGCTGAAGG 780
QY 1070 TGTTCAGATGATAGACACAGACAGCAGGAAACGATTCTTTTGAAGACTCAAAAGCG 1129
DB 781 TGTTCAGAACATGACAAAGGATAACAGCGGGACCATTACCTCGAGGAGCTCAAAACAG 840
QY 1130 GTTTGAAGAGTCCGATCTGAATGGAATCAGAAATCAAGTCTCTCATGATGCGG 1189
DB 841 GGTTCGCAAGACAGCGGCGCCCAAGCTGTACAGACAGCGAAATGGAGAACTAATGGA 900
QY 1190 CTGATATCGACACAGTGTGTACATAGACTACGAGAAATTCCTAGCAGCAACCTTACA 1249
DB 901 CTGACGCTGACGGCAAGGGTTAATTGACTACGCAATTTCTGACCGCAACAGTGCATA 960
QY 1250 TGAACAAGATGGAGAGAGAGATTTCTGGTGGCTGATTTTCGACTTTGACAAAGACG 1309
DB 961 TGAACAACCTGGATAGAGAGACCACTTTTACACAGCATTCACAGTATTTTCGACAGG 1020
QY 1310 GAAGCGGTTATATCCCATCGATGAGCTTCAAGTGTGACAGAGATTTGGTCTATG 1369
DB 1021 ACAGCGGTTACATTACTAAGAAGAGCTTGAGCACGCTTGAAGGAGCAAGGTTTGTATG 1080
QY 1370 ATACACT--CTGGACGACATGATCAAGGAGATTGATCTTGACATGAGCGGAAGATCG 1426
DB 1081 ACCCGCATAAATCAAGACATCATCTCCGATGCCACTCTGACAAATGATGAAGATAG 1140
QY 1427 ATTTCTCGAGTTTACAGCAATGATGAGGAAGGAGATGGAGTTGGGAGAGCAGAACCA 1486
DB 1141 ATTATTACAGTTTGGGCGATGATGAGGAAGGAGCGCTGTTGCGCGGCAATGAACA 1200
QY 1487 TGATGAAGA 1495
DB 1201 TCAAGAAGA 1209

RESULT 5

US-08-459-444-20
 ; Sequence 0, Application US/08459444
 ; Patent No. 6121014
 ; GENERAL INFORMATION:
 ; APPLICANT: Koziel, Michael G.
 ; Desai, Nalini M.
 ; Lewis, Kelly S.
 ; Kramer, Vance C.
 ; Warren, Gregory W.
 ; Evola, Stephen V.
 ; Crossland, Lytle D.
 ; Wright, Martha S.
 ; Merlin, Ellis J.
 ; Lounis, Karen L.

TITLE OF INVENTION: METHOD FOR PRODUCING A PLANT-OPTIMIZED
 NUCLEIC ACID CODING SEQUENCE

NUMBER OF SEQUENCES: 94
 CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 6121014artis Agribusiness Biotechnology Research, Inc.
 STREET: 3054 Cornwallis Road
 CITY: Research Triangle Park
 STATE: NC
 COUNTRY: USA
 ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/459,444A

FILING DATE: 02-Jun-1995

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/951,715

FILING DATE: 25-SEP-1992

APPLICATION NUMBER: US 07/772,027

FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: Meigs, J. Timothy

REGISTRATION NUMBER: 38,241

REFERENCE/DOCKET NUMBER: S-18805/PI/CGC1577/CIP/DIV6

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919)541-8587

TELEFAX: (919)541-8689

INFORMATION FOR SEQ ID NO: /note "cdna sequence for maize
 pollen-specific calcium dependent protein kinase gene as
 disclosed in Figure 30."

SEQUENCE CHARACTERISTICS:

LENGTH: 1349 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cdna

HYPOTHETICAL: NO

FEATURE:

NAME/KEY: CDS

LOCATION: 3..1226

SEQUENCE DESCRIPTION: SEQ ID NO: 20:

US-08-459-444-20

Query Match 24.6%; Score 429.8; DB 3; Length 1349;
 Best Local Similarity 60.3%; Pred. No. 1.4e-99;
 Matches 729; Conservative 0; Mismatches 477; Indels 3; Gaps 1;

QY 290 TTCAGATCATGTCATCTCTGAGCATCCAAATCTTGTAGGATCAAGGACATTATG 349

Db 1 TGCAGATCATGACCACTCTCGGGCCAGCCCACTGTGGCCCTCCGCGGCGCTACG 60

QY 350 AAGATTCGGTGTGTTGTCATATGTTATGAGGTTTGTGAAGTGTGAGCTTTTGTATC 409

Db 61 AGSACAAGCAGACGCTGCACCTCGTCATGAGCTGTCCGCGGCGGAGCTTTCGAC 120

QY 410 GGATTTGTTCTTAAAGGTCATTTTAGTAGAGCGTGAAGCTGTCAAGCTTATTAAAGACGATTC 469
 Db 121 GCATCATCGCCCGGGCCAGTACACGAGCGCGCGCGAGCTGCTCGCGGCCATCG 180
 QY 470 TTGGTGTGTTGAGGCTTGTCATCTCTGGTGTATGATAGAGATCTCAACCTTGAGA 529
 Db 181 TGCAGATCGTGCACACTGCCCTCCATGGGGGTGATGCACCGGACATCAAGCCCGAGA 240
 QY 530 ATTTCTTTTIGATAGTCTTAAAGATGATGCTAAGCTTAAGCTACCGATTTTGGTTTGT 589
 Db 241 ACITCTCTGCTCAGCAAGGACGAGGACGCGCGCTCAAGGCCACCGACTTCGGCTCT 300
 QY 590 CTGCTTCTATAAGCCAGGACAAATATTATATGACGTAGTTGGAAGTCCGTACTATGTTG 649
 Db 301 CCGTCTCTTCTCAAGGAGGCGGAGCTGCTCAGGGACATCTCGGCAGCGCTACTACATCG 360
 QY 650 CACCAGAGGTGCTTAAAGAAATGTTATGGACCTGAATATAGATGTGTGAGTGTGGTGTGA 709
 Db 361 CGCCCGAGGTGCTCAGAGGAAAGTACGCGCCGAGCCGACATCTGGAGCTCGCGGTCA 420
 QY 710 TCCTCTACATTTTACTCAGCGGTGTTCCCTCCCTCTGGGCGAGAGTGTGATCTGGAATCT 769
 Db 421 TGCTCTACATCTTCTCGCGCGGTGCTCCCTCTGGGCGAGAGAACGAGACGGCATCT 480
 QY 770 TTAGACAGATATTGCAAGGGAAGTTAGATTTCAAATCTGACCCGTGCGCTACTATCTCAG 829
 Db 481 TCACCCCATCTCGCGAGGCGACCTTGACCTCTCCAGCGAGCCATGCCACACATCTCGC 540
 QY 830 AAGCTGCTTAAAGATTGATCTATAAATGCTCGAAAGGAGCCCCCAAGAAACGCAATTTCTG 889
 Db 541 CGGGAGCCCAAGGATCTCGTCAAGAAGATGCTCAACATCAACCCCAAGGAGCGCTCACGG 600
 QY 890 CTCATGAAGCCTTGTCTCACCCTGATGATGTCATGAACAAGCAGCACCAGCAAGCCCTC 949
 Db 601 CGTTCAGGTCTCAATCACTCCCATGGATCAAGAGACGAGCGCGCTGACACCGCCG 660
 QY 950 TTGATCCAGCAGTCTTATCTCGTCTTAAAGCAGTTTTCTCAAATGAATAAGATTAAAGAAA 1009
 Db 661 TTGACAAAGTTGTTCTCGACAGGCTCAAGCAGTTTCAGGGCCATGAACCAAGTTCAAGAA 720
 QY 1010 TGGCATTTAGGGTAAATGCTGAGAGACTTTCAGAGGAAGAAATTTGAGGTCTGAGGAAT 1069
 Db 721 CAGCATTTAGGATCATAGCTGGTGGCTATCCGAAGAGGAGATCACAGGCTGAAGGAGA 780
 QY 1070 TGTTCAGATGATAGACACAGCAACAGCGGACGATTTACTTTTGAAGAGCTCAAGCGG 1129
 Db 781 TGTTCAGACATGACAGAGGATACAGCGGGACCAATTCCTCGACGAGCTCAACACG 840
 QY 1130 GTTTGAAGAGAGTCGGATCTGAATGGAATCAAGAAATCAAGTCTCTCATGGATCGGG 1189
 Db 841 GGTTCGCAAGCAGCGGCGCCCAAGCTGTCAAGCAGCGGAATGGAGAACTAATGGAAGCAG 900
 QY 1190 CTGATATCGACACAGTGTGTACAAATAGACTACGGGAATTCCTAGCAGCAACCTTACACA 1249
 Db 901 CTGACCTGACGGCAACGGGTAAATTTACTACGAGAAATTCGTCAACCCCAAGCAAGTGCATA 960
 QY 1250 TGAACAAGATGGAGAGAGGAGATTTCTGGTGGCTGCATTTTCGGACTTTTGACAAAGAGC 1309
 Db 961 TGAACAACCTGGATAGAGAGGACACCTTTACACAGCATTCACAGTATTTTCGACAGGACA 1020
 QY 1310 GAAGCGGTTATATCACCATCGATGAGCTTCAGTCAAGTTCAGCAGAGTTTGGTCTATGTTG 1369
 Db 1021 ACAGCGGGTACATTTACTAAGAAGAGCTTGAGCAGCGCTTGAAGGAGCAAGGGTGTATG 1080
 QY 1370 ATACACCT---CTGGACGACATGATCAAGGAGATTGATCTTACAAATGACGGGAAGATCG 1426
 Db 1081 AGCCGATTAATAATCAAGAGACATCTCCGATGCCGACTCTGCATATGATGGAAGGATAG 1140
 QY 1427 ATTTCTCGGAGTTTACGAATGATGAGGAAAGAGATGGAGTTTGGGAGAACGACCAACA 1486
 Db 1141 ATATTTCAGAGTTTGTGGCGATGATGAGGAAAGGACGCTGGTGGCCGAGCCATGAACA 1200
 QY 1487 TGATGAAGA 1495

Db 1201 TCAGAGAGA 1209
| | | | |
Db 1 TGCAGATCATGACACACCTCTCCGGCCAGCCCAAGCTGTGGGCTCCGCGCGGTACG 60
QY 350 AAGATTCGGTGTGTTTCATATTTGTTAGAGTGTGTTGAAAGTGTGAGTGTGTTGATC 409
| | | | |
Db 61 AGGACAAGCAGAGCGTGCACCTCGTCATGGAGCTGTGCGCGGGGGAGCTCTTCGACC 120
| | | | |
QY 410 GGATGTTTCTAAAGGTCAATTTAGTGAGCGTGAAGCTGTCAAGCTTTATTAAAGAGATTC 469
| | | | |
Db 121 GCATCATGCGCGCGGCGGAGTACAGGAGCGCGCGCGGAGCTGTGCGCGGCATCG 180
| | | | |
QY 470 TTGGTGTGTTGAGGCTTGTCTCTTGTGTTGTTATGCATAGAGATCTCAACCTGAGA 529
| | | | |
Db 181 TGCAGATCGTGACACCTGCCACTCCATGGGGGTGATGACCGGGACATCAAGCCCGAGA 240
| | | | |
QY 530 ATTTCTTTGTGATAGTCTTAAAGATGATGCTAAAGCTTAAGCTTAAAGCTTAAAGCTTGT 589
| | | | |
Db 241 ACTTCTGCTGCTCAGCAAGGACGAGGCGCGCTCAAGGCCACCGACTTCGSCCTCT 300
| | | | |
QY 590 CTGCTCTTATAAGCCAGGACAATTTATGACGTTAGTTGGAAGTCCGTAATGTTG 649
| | | | |
Db 301 CCGTCTTCTTCAAGGAGGCGAGCTGCTCAGGGACATCGTCGGCAGCGCTACTACATCG 360
| | | | |
QY 650 CACCAGAGTGTCTAAAGAAATGTTATGACCTGAATAGATGTGTGGAGTGTGTTGTTA 709
| | | | |
Db 361 CGCCGAGGTGCTCAAGAGGAGTACGGCCGGAGGCGGACATCTGGAGCGTGGCGTCA 420
| | | | |
QY 710 TCCTCTACATTTACTCAGCGTGTCTCTCTCTGGCAGAGACTGAGTCTGGAATCT 769
| | | | |
Db 421 TGCCTACATCTCTCTCGCGCGTGCCTCTCTCTGGCAGAGAACGAGACGCACT 480
| | | | |
QY 770 TTAGACAGATATGCAAGGAGTGTAGATTTCAAAATGACCCCGTGGCTACTACTCTCAG 829
| | | | |
Db 481 TCACCGCATCTCTCGAGGCGAGCTTGACCTCTCCAGCGAGCGCATGGCCACACATCTCG 540
| | | | |
QY 830 AAGCTGCTAAAGATTTGATCTATAAATGCTCGAAGGAGCCCAAGAACGCAATTTCTG 889
| | | | |
Db 541 CGGAGCCAGGATCTCTGCAAGAGTGTCTCAAGATGCTCAACATCAACCCCAAGGCGGTCTCAG 600
| | | | |
QY 890 CTCATGAAGCCTGTGTCTACCCATGGATTTGCGATGAAGAAATTTGAGGTCTGAAGGAT 1069
| | | | |
Db 721 CAGCATTCAGGATCATGCTGGTGCCTATCGAAGAGAGATCAGAGGCTGAAGGAGA 780
| | | | |
QY 1070 TGTTCAGATGATAGACACAGACACAGCGGAACGATTACTTTTGAAGAGCTCAAGCGG 1129
| | | | |
Db 781 GTTTCAGAACATTCACAAGGATAACAGCGGACCATTTACCTCGACGAGCTCAACACG 840
| | | | |
QY 1130 GTTTCAGAGAGTCCGATCTGAATGATGGAATCAGAATCAAGTCTCTCATGATCGG 1189
| | | | |
Db 841 GGTTCGAAAGCAGCGGCCCAAGCTGTGACAGACGGAATGGAGAAATTAATGGAAGCAG 900
| | | | |
QY 1190 CTGATATCGACAACAGTGTGTACATAGACTACGGAGATTTCTAGCAGCAACCTTACACA 1249
| | | | |
Db 901 CTGAGCTGACGGCAACGGTTAATGACTACGAGGATTCGTACCCCAACAGTGCATA 960
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QY 1250 TGACAAGATGGAGAGAGGAGATCTGGTGGTGCATTTTTCGAGCTTTGACAAAGACG 1309
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Db 961 TCACAAATCTGGATAGAGAGAGCACCCTTTACACAGCATTCAGATTTTCGACAAAGGACA 1020
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QY 1310 GAAGCGGTATATCACCATCGATGAGCTTCAGTTCAGCTTGACAGAGTTTGTCTATGTG 1369
| | | | |
Db 1021 ACAGCGGTATACATTAATAAGAGAGCTTGAGCAGCGCTTGAAGGAGCAAGGGTTGTATG 1080
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QY 1370 ATACACCTT---CTGACGACATGATCAAGGAGATTTGATCTTGACAAATCAGGGAGATCG 1426
| | | | |

RESULT 6
US-09-547-422-20
; Sequence 0, Application US/09547422
; Patent No. 6320100
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; Desai, Nalini M.
; Lewis, Kelly S.
; Kramer, Vance C.
; Warren, Gregory W.
; Crossland, Lyle D.
; Wright, Martha S.
; Merlin, Ellis J.
; Launis, Karen L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; CORRESPONDENCE ADDRESS: INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; ADDRESS: No. 6320100artis Agribusiness Biotechnology Research, Inc.
; STREET: 3054 Cornwalis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/547,422
; FILING DATE: 11-Apr-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/459,595
; FILING DATE: 02-JUN-1995
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: S-18805H
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8587
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: /note= "cdna sequence for maize
; pollen-specific calcium dependent protein kinase gene as
; disclosed in Figure 30."
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1349 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3..1226
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-547-422-20
Query Match 24.6%; Score 429.8; DB 4; Length 1349;
Best Local Similarity 60.3%; Pred. No. 1.4e-99;
Matches 729; Conservative 0; Mismatches 477; Indels 3; Gaps 1;
QY 290 TTCAGATCATGATCTCTGAGCATCCAAATGTTGTTAGGATCAAGGAGACTTATG 349

Db 1081 ACGCGATAAATCAAGACATCACTCCGATGCCGACTCTGACAAATGATGAAGATAG 1140
 QY 1427 ATTTCGGAGTTACAGCAATGATGAGAAAGGAGATGGAGTTGGGAGAACGACCA 1486
 Db 1141 ATTATTCAGAGTTTGTGGCGATGATGAGAAAGGACGCTGTGGCCGAGCCATGAACA 1200
 QY 1487 TGATCAAGA 1495
 Db 1201 TCAGAGA 1209

RESULT 7

US-08-459-448A-26
 ; Sequence 26, Application US/08459448A
 ; Patent No. 5859336

GENERAL INFORMATION:

APPLICANT: Koziel, Michael G.
 APPLICANT: Desai, Nalini M.
 APPLICANT: Lewis, Kelly S.
 APPLICANT: Kramer, Vance C.
 APPLICANT: Warren, Gregory W.
 APPLICANT: Evola, Stephen V.
 APPLICANT: Crossland, Lyle D.
 APPLICANT: Wright, Martha S.
 APPLICANT: Merlin, Ellis J.
 APPLICANT: Launis, Karen L.
 APPLICANT: Rothstein, Steven J.
 APPLICANT: Bowman, Cindy G.
 APPLICANT: Dawson, John L.
 APPLICANT: Dunder, Erik M.
 APPLICANT: Pace, Gary M.
 APPLICANT: Suttie, Janet L.
 TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
 TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
 NUMBER OF SEQUENCES: 94
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: No. 5859336artis Corporation
 STREET: Patent & Trademark Dept., 520 White Plains
 STREET: Rd., POB 2005
 CITY: Tarrytown
 STATE: New York
 COUNTRY: USA
 ZIP: 10591-9005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/459,448A
 FILING DATE: 02-JUN-1995
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/951,715
 FILING DATE: 25-SEP-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/772,027
 FILING DATE: 04-OCT-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Pace, Gary M.
 REGISTRATION NUMBER: 40403
 REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (919)541-8582
 TELEFAX: (919)541-8689
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4162 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO

FEATURE:
 NAME/KEY: misc feature
 LOCATION: 1418..1427
 OTHER INFORMATION: /note= "start of mRNA"

FEATURE:
 NAME/KEY: exon
 LOCATION: 1481..2366

FEATURE:
 NAME/KEY: intron
 LOCATION: 2367..2451

FEATURE:
 NAME/KEY: exon
 LOCATION: 2452..2602

FEATURE:
 NAME/KEY: intron
 LOCATION: 2603..2690

FEATURE:
 NAME/KEY: exon
 LOCATION: 2691..2804

FEATURE:
 NAME/KEY: intron
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FEATURE:
 NAME/KEY: exon
 LOCATION: 2907..3075

FEATURE:
 NAME/KEY: intron
 LOCATION: 3076..3177

FEATURE:
 NAME/KEY: exon
 LOCATION: 3178..3304

FEATURE:
 NAME/KEY: intron
 LOCATION: 3305..3398

FEATURE:
 NAME/KEY: exon
 LOCATION: 3399..3498

FEATURE:
 NAME/KEY: intron
 LOCATION: 3499..3713

FEATURE:
 NAME/KEY: exon
 LOCATION: 3714..3811

FEATURE:
 NAME/KEY: promoter
 LOCATION: 1..1477

IDENTIFICATION METHOD: experimental
 OTHER INFORMATION: /partial
 OTHER INFORMATION: /function= "pollen-specific promoter region"

OTHER INFORMATION: /evidence= EXPERIMENTAL
 US-08-459-448A-26

Query Match 12.5%; Score 218; DB 2; Length 4162;
 Best Local Similarity 59.8%; Pred. No. 9.4e-46;
 Matches 365; Conservative 0; Mismatches 245; Indels 0; Gaps 0;

QY 142 TACCTTCTGGGAAAAGCTAGGCCAAATTTGGAAACACCTATCTCTGCACAG 201
 Db 1757 TACTCGATGGCAAGGAGCTCGGCGCGGCGAGCTGGCGGTGACCGACCTGTGCACGCAC 1816

QY 202 AATATCAACCTCCGCTAATACGGCTCGAATATCCGGAAGGAAAGCTCGTGTGTCGC 261
 Db 1817 CGGACGAGGCGGCGAGAAGCTGGCGTCAAGACGATCGGCGGCGGCGGCGGCGGCGG 1876

QY 262 GAGGATACGAGATGATGGCGTGAGATTCAGATCATGCATCATCTCTGAGCATCA 321
 Db 1877 GAGGACGTGACGACCTCGGCGGCGGAGTGACAGATCATGCCACCTCTCCGCCAGCC 1936

QY 322 AATGTTTGTAGGATCAAGGCGACTTATGAAGATTCGGTGTGTTTTCATATTTGTTATGGAG 381
 Db 1937 AAGTGTGTGGCTCCGCGGCGGTACGAGGACAAACGAGCGGTGCACCTCGTCATGGAG 1996

QY 382 GTTTGTGAAGGCGGTGAGCTTTTGTGATCGGATTTTCTTAAAGGTCATTTTATGAGCGT 441

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Db 1997 CTGTGCGCGGGGAGCTTTTCGACCGCATCTCGCCGGGGCCAGTACACGGAGCGC 2056
QY 442 GAAGCTCTCAAGCTTATTAAGACGATTCCTGGTGTCTTGTGAGGCTTGTCTATCTCTTGGT 501
Db 2057 GGCCTCGGAGGCTGTGCGGGCCATCGTCGAGATCGTGCACACTGCCACTCCATGGGG 2116
QY 502 GTTATGATGAGATCTCAACACCTGAGAAATTCCTTGTTCATGATCTCTAAAGATGATGCT 561
Db 2117 GTGATGACCGGACATCAAGCCCGGAGAACTCTCTGCTGTCTCAAGAGGAGGAGCGCG 2176
QY 562 AAGCTTAAGGCTACCGATTTTGTCTGTCTCTCTATAGCCAGGACATATTTATAT 621
Db 2177 CCGCTCAAGGCCACCGCTCTCGGCTCTCGGCTCTCTCTCAAGAGGAGGAGCTCTCAGG 2236
QY 622 GACGTAGTGGAGCTGCTACTGTATGTCACCGAGGCTGCTAAAGAAATGTTATGGACCT 681
Db 2237 GACATCTGCGCAGCGCTACTATCATCGCCCGAGGTGCTCAAGAGGAGTACGGCCCG 2296
QY 682 GAATAGATGTGAGTGTGCTGTGTTATCTCTACATTTTACTCAGCGGTGTTCTCTCC 741
Db 2297 GAGCCGACATCTGAGCGTGGGGCTCATGCTCTACATCTCTCTCGCGGGGCTGCTCC 2356
QY 742 TTCGGGCGAG 751
Db 2357 TTCGGGCGAG 2366

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RESULT 8

US-08-459-595A-26
Sequence 26, Application US/08459595A
Patent No. 6018104

GENERAL INFORMATION:

APPLICANT: Koziel, Michael G.
APPLICANT: Desai, Nalini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Crossland, Lytle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Launis, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 6018104artis Corporation
STREET: Patent & Trademark Dept., 520 White Plains
STREET: Rd., POB 2005
CITY: Tarrytown
STATE: New York
COUNTRY: USA

COMPUTER READABLE FORM:

ZIP: 10591-9005
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,595A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: 40403
REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV3
TELEPHONE: (919)541-8582
TELEFAX: (919)541-8689
INFORMATION FOR SEQ. ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 4162 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHEICAL: NO
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1418..1427
OTHER INFORMATION: /note= "start of mRNA"
FEATURE:
NAME/KEY: exon
LOCATION: 1481..2366
FEATURE:
NAME/KEY: intron
LOCATION: 2367..2451
FEATURE:
NAME/KEY: exon
LOCATION: 2452..2602
FEATURE:
NAME/KEY: intron
LOCATION: 2603..2690
FEATURE:
NAME/KEY: exon
LOCATION: 2691..2804
FEATURE:
NAME/KEY: intron
LOCATION: 2805..2906
FEATURE:
NAME/KEY: exon
LOCATION: 2907..3075
FEATURE:
NAME/KEY: intron
LOCATION: 3076..3177
FEATURE:
NAME/KEY: exon
LOCATION: 3178..3304
FEATURE:
NAME/KEY: intron
LOCATION: 3305..3398
FEATURE:
NAME/KEY: exon
LOCATION: 3399..3498
FEATURE:
NAME/KEY: intron
LOCATION: 3499..3713
FEATURE:
NAME/KEY: exon
LOCATION: 3714..3811
FEATURE:
NAME/KEY: promoter
LOCATION: 1..1477
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /partial
OTHER INFORMATION: /function= "pollen-specific promoter region"
OTHER INFORMATION: /evidence= EXPERIMENTAL

US-08-459-595A-26

Query Match 12.5%; Score 218; DB 3; Length 4162;
Best Local Similarity 59.8%; Pred. No. 9.4e-46;
Matches 365; Conservative 0; Mismatches 245; Indels 0; Gaps 0;

142 TACCTTCTGGGAAAAAGCTAGGCCAAGCGCAATTGGAACCACTATCTCTGCACAG 201
1757 TACTCGATGGGAGGAGCTCGGCGGGGAGTTCGCGTGACGACCTGTGCACGAC 1816
202 AATCAACCTCCGCTAATTACGCTGCAATCGATCCGGAAGCAAGCTGTGTGCGC 261
1817 CGGACGAGCGGCGGAGAGCTGGCGTGAAGACGATCGGAAGCGGAAGCTGGCGGCGC 1876
262 GAGGATACGAGAGATGATCGCTGAGATTCAGATCATGATCATCTCTGACATCCCA 321
1877 GAGGACGTGGACGAGCTGGCGGGGAGTGCAGATCATGACACCTCTCGGCGGCGC 1936
322 AATGTTGTTAGGATCAAGGAGCTTATGAGATTCGGTGTGTTGTTGTTATGTTATGAG 381
1937 AACGTGTGGGCTTCGCGGGCGCTACGAGCAAGCAGACGCTGCACCTGCTCATGAG 1996
382 GTTGTGAAGGTGTGAGCTTTTGTGATCGGATTTTCTTAAAGTCTATTTAGTGAGCGT 441
1997 CTGTGCGCGGCGGGGAGCTTTCGACCGCATCATCGCCCGGGCCAGTACACGAGCGC 2056
442 GAAGCTGTCAAGCTTATTAAAGCATTTCTTGGTCTGTTGAGGCTTGTCTCTCTTGGT 501
2057 GCGCGCGGAGCTGTGCGGGCGCATGTCGAGATCTGACACCTGCGCATCTCATGGG 2116
502 GTTATGATAGATCTCAACCTGAGAACTTCTTGTGATAGTCTCTAAAGATGATGCT 561
2117 GTGATGACCGGACATCAAGCCCGGAACTTCTGCTGCTCAAGAGGAGGAGCGG 2176
562 AAGCTTAAGCTACGATTTTGTGTTCTGCTCTCTCTATTAAGCCAGGACAAATTTATAT 621
2177 CCGCTCAAGGCCACCGACTTGGGCTCTCGGCTCTCTCTCTCAAGGAGGAGGCTGCTCAGG 2236
622 GACGTAGTGGAGCTCGTACTATGTTGACACGAGTGTCTAAAGAAATGTTATGGACCT 681
2237 GACATGCTGCGCAGCGCTACTACATCGCGCCGAGTGTCTCAAGAGGAGTACGCGCGG 2296
682 GAAATAGATGTGGAGTGTGGTGTGTTATCTCTACATTTTACPCAGCGGTGTTCCTCC 741
2297 GAGCGCGACATCTGAGCGTGGGCTGATGCTCTACATCTCTCTCGCGGCGGTGCTCC 2356
742 TTCTGGGCGAG 751
2357 TTCTGGGCGAG 2366

RESULT 9

US-08-459-504B-26

Sequence 26, Application US/08459504B

Patent No. 6075185

GENERAL INFORMATION:

APPLICANT: Koziel, Michael G.
APPLICANT: Desai, Nalini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Launis, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.

TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED

TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 6075185artis Corporation

STREET: 3054 Cornwallis Road

CITY: Research Triangle Park

STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,504B
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/459,595
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC1577/CIP/DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 4162 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1418..1427
OTHER INFORMATION: /note= "start of mRNA"
NAME/KEY: exon
LOCATION: 1481..2366
FEATURE:
NAME/KEY: intron
LOCATION: 2367..2451
FEATURE:
NAME/KEY: exon
LOCATION: 2452..2602
FEATURE:
NAME/KEY: intron
LOCATION: 2603..2690
FEATURE:
NAME/KEY: exon
LOCATION: 2691..2804
FEATURE:
NAME/KEY: intron
LOCATION: 2805..2906
FEATURE:
NAME/KEY: exon
LOCATION: 2907..3075
FEATURE:
NAME/KEY: intron
LOCATION: 3076..3177
FEATURE:
NAME/KEY: exon
LOCATION: 3178..3304
FEATURE:
NAME/KEY: intron
LOCATION: 3305..3398
FEATURE:
NAME/KEY: exon
LOCATION: 3399..3498
FEATURE:

NAME/KEY: intron
LOCATION: 3499..3713
FEATURE:
NAME/KEY: exon
LOCATION: 3714..3811
US-08-459-504B-26

Query Match 12.5%; Score 218; DB 3; Length 4162;
Best Local Similarity 59.8%; Pred. No. 9.4e-46;
Matches 365; Conservative 0; Mismatches 245; Indels 0; Gaps 0;

Qy 142 TACCTTCGGAAGAAAGCTAGGCGCAATTTGGAACAACCTATCTCTGCACAG 201
Db 1757 TACTCGATGGCAGAGGAGCTCGGCGCGGAGTTGCGCGTACGACCTGTGCACGAC 1816
Qy 202 AAATCAACCTCCGTAAATAGCCCTGCAATCGATCCGGAAGAAAGCTGTGTGCGC 261
Db 1817 CGGACGAGCGGCGAAGCTGGCGTGAAGACGATCGCGAAGCGAAGCTGCGCGCCAGG 1876
Qy 262 GAGGATACGAAGATGATGCGCTGAGATTCAGATCATGATCTCTCTGAGCATCCA 321
Db 1877 GAGGACGTGGAGCGAGCTGCGCGGAGGAGTGCAGATCATGACCAACCTCTCGCGGCGAGCC 1936
Qy 322 AATCTTGTAGGATCAAGGACCTTATGAAGATTCGGTGTGTTCATATGTTATGGAG 381
Db 1937 AACGTGTGGGCTCCGCGGCGGTACGAGCAGCAGAGCGTGACCTCTGATGGAG 1996
Qy 382 GTTGTGAAGTGTGAGCTTTTGTATCGGATTTGTTTAAAGTCAATTTTGTAGTACGCT 441
Db 1997 CTGTGCGCGGCGGAGCTCTTCGACCGCATCATCGCGCGGCGGCGGCGGCGGCG 2056
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Db 2057 GCGCGCGGAGCTGCTGCGGCGCATGTCGAGATCTGTGACACCTGCGCTCCATGGG 2116
Qy 502 GTTATGATAGATCTCAACCTGAGAACTTCTTGTGTATGATCTCTAAAGATGATGCT 561
Db 2117 GTGATGACCGGAGCATCAAGCCGAGAACTTCTGCTGCTCAGCAGGAGGAGCGG 2176
Qy 562 AAGCTTAAGCTACCGATTTTGTCTGTCTGTCTATAGCCAGCAGACATATTTAT 621
Db 2177 CCGCTCAAGCCACCGCTCTCGGCTCTCTCTCTCTCTCAAGGAGGCGGAGCTCTCAGG 2236
Qy 622 GAGTATGTGAGTCCGCTACTATGTTCACGAGGCTGCTAAAGAAATGTATGGACCT 681
Db 2237 GACATCTCGCAGCGCTACTATCTGCTGCGCGGAGTGTCAAGAGAGTACGCGCGG 2296
Qy 682 GAATAGATGTGAGTGTGTGTATCTCTTACATTTTACTCAGCGGTGTCTCTCC 741
Db 2297 GAGCGCGACATCTGAGCGCTCGGCGTCTGCTCTACATCTCTCTCTCTCTCTCTCC 2356
Qy 742 TTCTGGGCGAG 751
Db 2357 TTCUGGCGAG 2366

RESULT 10
US-08-459-444-26
Sequence 26, Application US/08459444
Patent No. 6121014
GENERAL INFORMATION:
APPLICANT: Kozie, Michael G.
Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Launis, Karen L.
TITLE OF INVENTION: METHOD FOR PRODUCING A PLANT-OPTIMIZED
NUCLEIC ACID CODING SEQUENCE

NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6121014artis Agribusiness Biotechnology Research, Inc.
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,444A
FILING DATE: 02-Jun-1995
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-18805/P1/GC1577/CIP/DIV6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 4162 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1418..1427
OTHER INFORMATION: /note= "start of mRNA"
FEATURE:
NAME/KEY: exon
LOCATION: 1481..2366
FEATURE:
NAME/KEY: intron
LOCATION: 2367..2451
FEATURE:
NAME/KEY: exon
LOCATION: 2452..2602
FEATURE:
NAME/KEY: intron
LOCATION: 2603..2690
FEATURE:
NAME/KEY: exon
LOCATION: 2691..2804
FEATURE:
NAME/KEY: intron
LOCATION: 2805..2906
FEATURE:
NAME/KEY: exon
LOCATION: 2907..3075
FEATURE:
NAME/KEY: intron
LOCATION: 3076..3177
FEATURE:
NAME/KEY: exon
LOCATION: 3178..3304
FEATURE:
NAME/KEY: intron
LOCATION: 3305..3398
FEATURE:
NAME/KEY: exon

LOCATION: 3399..3498
FEATURE:
NAME/KEY: intron
LOCATION: 3499..3713
FEATURE:
NAME/KEY: exon
LOCATION: 3714..3811
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-08-459-444-26

Query Match 12.5%; Score 218; DB 3; Length 4162;
Best Local Similarity 59.8%; Pred. No. 9.4e-46;
Matches 365; Conservative 0; Mismatches 245; Indels 0; Gaps 0;

QY 142 TACCCTCTGGGAAAAGCTAGCCCAAGCCCAATTGGGAACACCTATCTCTGCACAG 201
DB 1757 TACTCATGGGAAGAGCTGGCGGGGAGTTCGGGGTACCGACCTGTGCACGCAC 1816
QY 202 AATCAACCTCCGCTAATACGCTCAAAATCGATCCCGAAGCAAGCTCGTGTGTCG 261
DB 1817 CGGACGAGCGCGAGAGCTGGCTGCAAGACGATCGCGAGGAGTGGGGCCAGG 1876
QY 262 GAGGATTACAGATGATGCGGTGAGATTGATGATCATCATCATCTCTGAGCATCCA 321
DB 1877 GAGGAGCTGGAGCAGCTGGCGGGGAGTCCAGATCATCATCATCTCTCGGCCAGCC 1936
QY 322 AATGTGTTAGGATCAAGGGGACTTATGAAGATTGCGTGTGTTTCATATTGTTAGG 381
DB 1937 AACGTGTTGGGCTCGCGGGGCTGACGAGGACAGCAGCGTGCACCTCGTCATGGAG 1996
QY 382 GTTGTGAAGGTGGTGGAGCTTTTGTGATCGGATGTTTCTTAAAGGTCAATTTAGTACG 441
DB 1997 CTCTGCGCGGGGGAGCTCTCGACCGCATCATCGCCCGGGGCCAGTACACGGAGCG 2056
QY 442 GAAGCTGCAAGCTTATTAAGAGATCTTGTGTTGTTGAGCTTGTCTATCTCTGTGT 501
DB 2057 GCGCGCGGAGCTGCTGCGGCCATCTGTCAGATGTCGACACCTGCCACTCCATGGGG 2116
QY 502 GTATGATAGAGATCTCAAACTGAGAATTTCTTTGTAGTCTCTAAAGATGATGCT 561
DB 2117 GTGATCACCAGGACATCAAGCCCGAGACTTCTGCTCTCAGCAGGACGAGGACGG 2176
QY 562 AAGCTTAAGCTAACGATTTTGGTTGTGCTGCTCTTCTTAAGCAGGACAAATATTATAT 621
DB 2177 CCGCTCAAGGCGACGACTTCGCGCTCTCCGCTCTTCTTCAAGAGGCGGAGCTGCTCAG 2236
QY 622 GAGCTAGTTGAAGTCCGCTACTATGTTGACACGAGGCTCTAAAGAAATGTTATGACCT 681
DB 2237 GACATGCTCGGACGCGCTACTACATCGCGCCGAGTCTCAAGAGGAGTACGCGCG 2296
QY 682 GAAATAGATGTTGAGTCTGGTGTATTCCTCTACATTTTACTCAGCGGTGTTCTCC 741
DB 2297 GAGGCGGACATCTGGAGCGTGGCGCTCATCTCTACATCTCTCTCGCGCGTGTCTCC 2356
QY 742 TTCTGGGCAG 751
DB 2357 TTCTGGGCAG 2366

RESULT 11

US-09-547-422-26
Sequence 26, Application US/09547422
Patent No. 6320100
GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.

Launis, Karen L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESS: No. 6320100artis Agribusiness Biotechnology Research, Inc.
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/547,422
FILING DATE: 11-Apr-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/459,595
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-18805H
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 4162 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: misc feature
LOCATION: 1418..1427
OTHER INFORMATION: /note= "start of mRNA"
FEATURE:
NAME/KEY: exon
LOCATION: 1481..2366
FEATURE:
NAME/KEY: intron
LOCATION: 2367..2451
FEATURE:
NAME/KEY: exon
LOCATION: 2452..2602
FEATURE:
NAME/KEY: intron
LOCATION: 2603..2690
FEATURE:
NAME/KEY: exon
LOCATION: 2691..2804
FEATURE:
NAME/KEY: intron
LOCATION: 2805..2906
FEATURE:
NAME/KEY: exon
LOCATION: 2907..3075
FEATURE:
NAME/KEY: intron
LOCATION: 3076..3177
FEATURE:
NAME/KEY: exon
LOCATION: 3178..3304

APPLICANT:	Warren, Gregory W.
APPLICANT:	Evola, Stephen V.
APPLICANT:	Crossland, Lyle D.
APPLICANT:	Wright, Martha S.
APPLICANT:	Merlin, Ellis J.
APPLICANT:	Launis, Karen L.
APPLICANT:	Rothstein, Steven J.
APPLICANT:	Bowman, Cindy G.
APPLICANT:	Dawson, John L.
APPLICANT:	Dunder, Erik M.
APPLICANT:	Pace, Gary M.
APPLICANT:	Suttie, Janet L.
TITLE OF INVENTION:	SYNTHETIC DNA SEQUENCE HAVING ENHANCED INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES:	94
CORRESPONDENCE ADDRESS:	
ADDRESSEE:	CIBA-GEIGY Corporation
STREET:	7 Skyline Drive
CITY:	Hawthorne
STATE:	New York
COUNTRY:	USA
ZIP:	10532
COMPUTER READABLE FORM:	
MEDIUM TYPE:	Floppy disk
COMPUTER:	IBM PC compatible
OPERATING SYSTEM:	PC-DOS/MS-DOS
SOFTWARE:	PatentIn Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:	
APPLICATION NUMBER:	US/07/951,715A
FILING DATE:	25-SEP-1992
CLASSIFICATION:	800
PRIOR APPLICATION DATA:	
APPLICATION NUMBER:	US 07/772,027
FILING DATE:	04-OCT-1991
ATTORNEY/AGENT INFORMATION:	
NAME:	Spruill, W. Murray
REGISTRATION NUMBER:	32,943
REFERENCE/DOCKET NUMBER:	S-18805/A/CGC 1577/CIP
TELECOMMUNICATION INFORMATION:	
TELEPHONE:	(919)541-8615
TELEFAX:	(919)541-8689
INFORMATION FOR SEQ ID NO:	26:
SEQUENCE CHARACTERISTICS:	
LENGTH:	4165 base pairs
TYPE:	nucleic acid
STRANDEDNESS:	single
TOPOLOGY:	linear
MOLECULE TYPE:	DNA (genomic)
HYPOTHETICAL:	NO
FEATURE:	
NAME/KEY:	misc_feature
LOCATION:	1416..1425
OTHER INFORMATION:	/note= "start of mRNA"
NAME/KEY:	exon
LOCATION:	1481..2366
FEATURE:	
NAME/KEY:	intron
LOCATION:	2367..2449
FEATURE:	
NAME/KEY:	exon
LOCATION:	2450..2602
FEATURE:	
NAME/KEY:	intron
LOCATION:	2603..2688
FEATURE:	
NAME/KEY:	exon
LOCATION:	2689..2804
FEATURE:	
NAME/KEY:	intron
LOCATION:	2805..2906
FEATURE:	
NAME/KEY:	exon

LOCATION: 2907...3074
FEATURE:
NAME/KEY: intron
LOCATION: 3075...3177
FEATURE:
NAME/KEY: exon
LOCATION: 3178...3305
FEATURE:
NAME/KEY: intron
LOCATION: 3306...3397
FEATURE:
NAME/KEY: exon
LOCATION: 3398...3497
FEATURE:
NAME/KEY: intron
LOCATION: 3498...3712
FEATURE:
NAME/KEY: exon
LOCATION: 3713...3811
US-09-951-715A-26

Query Match 12.5%; Score 218; DB 1; Length 4165;
Best Local Similarity 59.8%; Pred. No. 9.4e-46;
Matches 365; Conservative 0; Mismatches 245; Indels 0; Gaps 0;
QY 142 TACCTTCTGGGAAAGGCTAGGCCAAGGCCAATTTGSAACAACCTATCTCTGCACAGAG 201
DB 1755 TACTCGATGGCAAGGAGCTCGGCGGGGAGTTTCGGCGTGAGCGACCTGTGCACGCAC 1814
QY 202 AAATCAACCTCCGCTAATTACGCTCGCAATCGATCCCGAAGCAAGCTCGTGTGTCG 261
DB 1815 CGGACGAGCGGAGAGCTGGCGTGCAAGACGATCGCGAAGCGAAGCTGGCGGCAGG 1874
QY 262 GAGGATTACGAAGATGATGCGCTGAGATTCAGATCATGATCATCTCTGAGCATCCA 321
DB 1875 GAGGACGTGACGAGCTGCGCGGGAGTGCGAGATCATGACCACTCTCGGGCCAGCC 1934
QY 322 AATCTTGTAGGATCAAGGACTTATGAAGATTCGCTGTTGTTTCATATGTTATGGAG 381
DB 1935 AACGTGTGGCCCTCCGCGGCGGTACGAGGACCAAGCAGCGGTGCACTCGTCATGGAG 1994
QY 382 GTTGTGAAGGTGTGAGCTTTTGTGATCGGATTTGTTCTAAAGGTCAATTTTGTGAGCGT 441
DB 1995 CTGTGCGCGCGGGAGCTCTTCGACCGCATCATCGCCGGGCCAGTACACGAGCGC 2054
QY 442 GAAGCTGCAAGCTTATTAAGACGATCTTGGTGTTGTGAGGCTGTGATCTCTTGGT 501
DB 2055 GCGCGCGGAGCTGCTGCGCGCCATCGTGCAGATCGTGCACACTGCGCACTCCATGGG 2114
QY 502 GTTATGATAGATCTCAAACTGAGAAATTTCTTTGTTGATAGTCTCTAAAGATGATGCT 561
DB 2115 GTGATGACCGGACATCAAGCCGAGACTTCTGCTGCTCAGCAGGAGGAGCGCG 2174
QY 562 AAGCTTAAGCTACCGATTTTGGTTGTCTGCTTCTATTAAGCAGGACAAATTTATAT 621
DB 2175 CCGCTCAAGGCCACCGACTTCGGCTCTCCGCTCTCTTCTCAAGGAGGCGAGCTGCTCAGG 2234
QY 622 GACCTAGTGAAGTCGCTACTATGTCCACAGAGGTGCTTAAGAAATGTTATGAGCT 681
DB 2235 GACATGCTGCGACGGCTACTATACATCGCCGCGAGTGTCTCAAGAGGAAGTACGGCCG 2294
QY 682 GAAATAGATGTGTGAGTGTGTTATCTCTACATTTTACTCAGCGGTGTTCTCC 741
DB 2295 GAGGCCGACATCTGGAGCTCGGCTGCTATGCTCTACATCTCTCCGCGGCGCTCC 2354
QY 742 TTCTGGGCGAG 751
DB 2355 TTCGGGCGAG 2364

RESULT 13
US-09-347-801-3
; Sequence 3, Application us/09347801

Patent No. 6262345
GENERAL INFORMATION:
APPLICANT: Allen, Steve
TITLE OF INVENTION: Plant Protein Kinases
FILE REFERENCE: BB-1171
CURRENT APPLICATION NUMBER: US/09/347,801
EARLIER APPLICATION NUMBER: 60/092,438
EARLIER FILING DATE: July 10, 1998
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Microsoft Office 97
SEQ ID NO 3
LENGTH: 2374
TYPE: DNA
ORGANISM: Oryza sativa
US-09-347-801-3

Query Match 10.9%; Score 189.6; DB 4; Length 2374;
Best Local Similarity 53.8%; Pred. No. 1.2e-38;
Matches 440; Conservative 0; Mismatches 369; Indels 9; Gaps 2;
QY 271 GAAGATGATGGCGTGAGATTCAGATCATGATCATCTCTGAGCATCCAAATGTTGTT 330
DB 846 GAGGATTTCTGTAGAGAAGTAAATTTTGAGAGCGTTATCAGGCGCAATAATCTCGTC 905
QY 331 AGGATCAAGGGAGCTTATGAAGATTCGGTGTTCCTCATATTTGATGGAGTTTGAA 390
DB 906 AATTCATGATGATGAGATGGCTCAATGCTACATGTCATGGAATTAATGTAG 965
QY 391 GGTGGTGAAGTTTGTATCGGATTTCTTAAAGTCAATTTAGTGAGCGTGAAGCTGC 450
DB 966 GGAGGAGATTTGCTAGACAGAAATATTAGCCAGAGCGGGAGATACACAGAGGAAGTGC 1025
QY 451 AA---GCTTATTAAGAGATTTCTGTTGTTGAGCTGTGAGCTTCTGAGGGGTAGT 1085
DB 1026 AAAGCGATTTGTTACAGATTTTGAAGCTGTGAGCTTCTGATCTCTGAGGGGTAGT 1085
QY 508 CATAGATCTCAACCTGAGAAATTTCTGTTGATAGTCTCTAAGATGATGCTAAGCTT 567
DB 1086 CATGCTGATTGAAGCCAGAGAAATTTCTTTTCAACACCGAGGATGAATGCTCCCATG 1145
QY 568 AAGCTACCGATTTGCTGCTCTCTTATAAGCCAGGACAAATATTATATGAGCTA 627
DB 1146 AAGTTGATTTGTTGCTCTGATTTTCAATAGACAGATGAAGCGCTTAATGATATT 1205
QY 528 GTTGAAGTCCGTACTATGTTGACAGAGGTGCTAAAGAAATTTATGACCTGAAATA 687
DB 1206 GTTGAAGTGCATATTATGTTGCCAGAGGTTTACACAGATCATATAGTATGGAAGCA 1265
QY 588 GATGTGGAGTGTGTTGTTATCTCTACATTTTACTCAGCGGTGTTCTCCCTCTCGG 747
DB 1266 GACATTTGGAGTATAGGTGTCATAACGTACTCTGCTGTGCGCAGTCGCGCATCTCG 1325
QY 748 GCAGAGACTGAGTCTGGAATCTTTAGACAGATATTGCAAGGGAAGTTAGATTTCAATCT 807
DB 1326 GCAGACAGATCAGGAATATTCGGATCTGTGTGAGAGCTGATCCCACTTTGATGAT 1385
QY 808 GACCGGTGGCTACTATCTCAGAGCTGCTAAAGATTTGATCTATAAAATGCTCGAAAG 867
DB 1386 TCACCGTGGCTACAGTATCAGCTGAAGCTAAGGATTTTGTGAAGAGATTTCTCAACAA 1445
QY 868 AGCCCCAAGAAACGATTTCTGCTCATGAGCGCTTGTGTCACCCATGATGTCGATGAA 927
DB 1446 GATTACCGCAAAAGAAATGACCGTGTTCAGAGCACTGACTCATCTTGTGTCGAGATGAA 1505
QY 928 CAAGCAGCCAGCAGACCTCTTGATCCAGAGCTCTTATCTGCTTAAAGAGCTTTCT 987
DB 1506 CA-----AAGGAGATCCCGCTGGACATCTCATCTTCAGATTAATTAAGCAATACCT 1559
QY 988 CAATGAATGAATTAAGAAATAGGCTTACGGGTAATTCGTCAGACCTTTTCAGAGGAA 1047
DB 1560 CGCGCTACACCTCTTAACGGTTGGCATTAAGGCATATCCAGAGGCTTTAAGGGAAGAT 1619

RESULT 15
US-08-338-057-1
Sequence 1, Application US/08338057
Patent No. 5795741
GENERAL INFORMATION:
APPLICANT: Tomley, Fiona M.
APPLICANT: Dunn, Paul P. J.
APPLICANT: Bumstead, Janene M.
APPLICANT: Vermeulen, Arno N.
TITLE OF INVENTION: Coccidiosis poultry vaccine
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Organon Teknika Corporation
STREET: 1330 Piccard Drive
CITY: Rockville
STATE: Maryland
COUNTRY: U.S.A.
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/338,057
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93.309078.9
FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Gormley, Mary E.
REGISTRATION NUMBER: 34,409
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 258-5200
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

LENGTH: 1400 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: C-terminal
ORIGINAL SOURCE:

ORGANISM: Eimeria maxima
STRAIN: Houghton
DEVELOPMENTAL STAGE: sporozoite
IMMEDIATE SOURCE:
LIBRARY: sporozoite cDNA cloned in Lambda ZAPII
CLONE: Em70-1

FEATURE:
NAME/KEY: CDS
LOCATION: 1..1368
US-08-338-057-1

Query Match 9.4%; Score 165; DB 1; Length 1400;
Best Local Similarity 54.5%; Pred. No. 1.6e-32;
Matches 330; Conservative 0; Mismatches 275; Indels 0; Gaps 0;

QY 313 GAGCATCCAAATGTTGTAGCATCAAGGGACATTATGAAGATTCCGGTGTGTTTCATATT 372
DB 151 GATCATCCTAATATCAAGAAATTATGAATCTTTGAGGATAAGGATACCTTTTATCTT 210

QY 373 GTTATGAGGTTTGTGAAGGTGGTGAAGTTTGTGCGGATGTTTCTAAAGGTCATTTT 432
DB 211 GTTACAGAAGTATATACAGGAGGAGAAATTATTTGATGAATTTATTAATCCAAAAGATTC 270

QY 433 AATGAGGCTGAAGCTGTCAAGCTTATTAAGCAGATTCCTGGTGTGTTGAGGCTTGTCTAT 492
DB 271 AGCGAGGCGGATCAGCTCGCTATAGTACGTCAGGTTCTATCGGGTATATAATTATATGCAI 330

QY 493 TCTCTGGTGTATGATAGATCTCAACCTGAGAAATTTCTTTGATAGTCTCTAAA 552
DB 331 CGTAATAAATAGTTCATAGAGATTTAAAGCCAGAGAAATTTATTAGAGAAATAAAAA 390

QY 553 GATGATGCTAAGCTTAAGGCTACCGATTTTGGTGTGTTCTCTCTCTATAAGCCAGGACAA 612
DB 391 AAAGATGCAAAATATAGAAATTTATGATTTTGGGTATCTACACATTTTGAGCCCAAAAA 450

QY 613 TATTTATGACGCTAGTGTGAGTCCGTACTATGTCACCCAGAGGTGCTAAAGAAATGT 672
DB 451 AATGAAGGATAAATCGGGACCGGCTACTACATTGCCCCCTGAGGTGCTGCACGGAACA 510

QY 673 TATGACCTGAATAGATGTGAGTGTGTTGTTATCTCTACATTTTACTCAGCGGT 732
DB 511 TAGGATGAGAAATGCGACGCTGCTGCTACGGGTGTTATCTCTATATCTCTCTCTGTT 570

QY 733 GTTCCCTCCCTTTGCGGAGAGATGAGTCTGGAATCTTTAGACAGATATTGCAAGGGAAG 792
DB 571 TGTCTCCCAATTAACGGAGCAAAATGAATTTGAAATTTCTAAAGAAAGTCGAGAAAGGAAA 630

QY 793 TTAGATTTCAAATCTGACCGCTGGCTACTATCTCAGAGAGCTCTAAAGATTTGATCTAT 852
DB 631 TTCACCTTCGATTTACACAGTGGCGTAGGTTAGCGAGCCAGCAAAAGATTTAAATAGG 690

QY 853 AAAATGCTGAAAGAGGCCCCAGAAACGATTTCTGCTCATGAAGCTTGTCTCACCCA 912
DB 691 AAGATGTTAGCATATGTACCCTCAATCGGTATATACGAAAGATGCAATAGATCATCCA 750

QY 913 TGGAT 917
DB 751 TGGAT 755

Search completed: March 26, 2003, 06:39:04
Job time : 147 secs

GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: March 26, 2003, 08:01:19 ; Search time 475 Seconds

(Without alignments)
3129.789 Million cell updates/sec

Title: US-09-848-806-2

Perfect score: 1747

Sequence: 1 gatccgggtacatatcttc.....tataaaagttttgaattcc 1747

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 574371 seqs, 425486471 residues

Total number of hits satisfying chosen parameters: 1148742

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published_Applications_NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
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- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
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- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1484.8	85.0	1488	9	US-09-938-842A-704
2	744.2	42.6	1473	9	US-09-938-842A-786
3	712.6	40.8	1635	9	US-09-938-842A-2344
4	643.4	36.8	1833	9	US-09-938-842A-2334
5	531.8	30.4	2230	10	US-09-828-313-26
6	507.8	29.1	1638	9	US-09-938-842A-1859
7	448.2	25.7	455	10	US-09-770-444-571
8	444.6	25.4	1602	9	US-09-938-842A-2304
9	429.8	24.6	1349	9	US-09-988-462-20
10	277.8	15.9	1387	10	US-09-828-313-13
11	227.4	13.0	955	10	US-09-770-445-326
12	221.6	12.7	2253	10	US-09-828-313-25
13	218	12.5	4162	9	US-09-988-462-26
14	200.6	11.5	1800	9	US-09-938-842A-1063
15	193	11.0	718	9	US-09-938-842A-3678
16	189.6	10.9	2374	10	US-09-854-731-3
17	168	9.6	413	10	US-09-878-574-3809
18	159.6	9.1	1372	10	US-09-817-181-1
19	155	8.9	267	10	US-09-923-876-331

20 145.6 8.3 1074 9 US-10-024-036B-3 Sequence 3, Appli

21 145.6 8.3 1578 10 US-09-835-788A-6 Sequence 6, Appli

22 145.6 8.3 1772 9 US-10-024-036B-1 Sequence 1, Appli

23 142.4 8.2 275 10 US-09-878-574-13205 Sequence 13205, A

24 141.8 8.1 1158 9 US-10-116-332-1 Sequence 1, Appli

25 141.8 8.1 7626 9 US-09-917-800A-1537 Sequence 82, Appli

26 133.6 7.6 5637 10 US-09-001-835-82 Sequence 1537, Ap

27 122 7.0 281 10 US-09-294-093B-3885 Sequence 3885, Ap

28 121.4 6.9 1383 9 US-09-935-464-2 Sequence 2, Appli

29 121.4 6.9 1738 9 US-09-935-464-4 Sequence 4, Appli

30 117 6.7 2061 12 US-10-096-960-1 Sequence 1, Appli

31 117 6.7 3705 12 US-10-044-090-227 Sequence 227, App

32 114.2 6.5 457 9 US-09-796-692-7777 Sequence 7777, Ap

33 112 6.4 247 10 US-09-878-574-7818 Sequence 7818, Ap

34 111.8 6.4 1551 9 US-09-925-299-210 Sequence 210, App

35 111.8 6.4 1551 10 US-09-925-299-210 Sequence 210, App

36 106.2 6.1 260 10 US-09-878-574-9200 Sequence 9200, Ap

37 105.6 6.0 270 10 US-09-294-093B-4541 Sequence 4541, Ap

38 105.6 6.0 1539 9 US-09-938-842A-162 Sequence 162, App

39 104.8 6.0 855 9 US-09-938-842A-2190 Sequence 2190, Ap

40 100 5.7 1539 9 US-09-938-842A-2657 Sequence 2657, Ap

41 99.4 5.7 1167 10 US-09-940-921B-6 Sequence 6, Appli

42 99.4 5.7 1197 10 US-09-940-921B-8 Sequence 8, Appli

43 99.4 5.7 1744 10 US-09-940-921B-10 Sequence 10, Appli

44 92.6 5.3 498 10 US-09-854-731-7 Sequence 7, Appli

45 91.6 5.2 174 10 US-09-294-093B-5432 Sequence 5432, Ap

ALIGNMENTS

RESULT 1

US-09-938-842A-704

; Sequence 704, Application US/09938842A

; Patent No. US20020160378A1

; GENERAL INFORMATION:

; APPLICANT: Harper, Jeff

; APPLICANT: Kreps, Joel

; APPLICANT: Wang, Xun

; APPLICANT: Zhu, Tong

; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAININ

; FILE REFERENCE: SAME, AND METHODS OF USE

; CURRENT APPLICATION NUMBER: US/09/938,842A

; CURRENT FILING DATE: 2001-08-24

; PRIOR APPLICATION NUMBER: US 60/227,866

; PRIOR FILING DATE: 2000-08-24

; PRIOR APPLICATION NUMBER: US 60/264,647

; PRIOR FILING DATE: 2001-01-16

; PRIOR APPLICATION NUMBER: US 60/300,111

; PRIOR FILING DATE: 2001-06-22

; NUMBER OF SEQ ID NOS: 5379

; SEQ ID NO 704

; LENGTH: 1488

; TYPE: DNA

; ORGANISM: Arabidopsis thaliana

US-09-938-842A-704

Query Match 85.0%; Score 1484.8; DB 9; Length 1488;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1488; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 67 ATGGAGACGAGCCAAACCCCTAGACGTCCTTCAAACACAGCTTCTACCATATCAACACCA 126

Db 1 ATGGAGACGAGCCAAACCCCTAGACGTCCTTCAAACACAGCTTCTACCATATCAACACCA 60

QY 127 CGATTAGACATCATTACCTTCTGGGAAAAAGCTAGCCAAAGCCCAATTGGAAACAAC 186

Db 61 CGATTAGACATCATTACCTTCTGGGAAAAAGCTAGCCAAAGCCCAATTGGAAACAAC 120

QY 187 TATCTCTGCACAGAGAAATCAACCTCGGCTAANTACGCTTGAATTCGATCCCGAGAGCG 246

Db 121 TATCTCTGCACAGAGAAATCAACCTCGGCTAANTACGCTTGAATTCGATCCCGAGAGCG 180

QY 247 AAGTCGCTGTGCGGAGGATTACGAAGATGATGGCTGAGATTCAGATCATGATCAT 306
Db 181 AAGTCGCTGTGCGGAGGATTACGAAGATGATGGCTGAGATTCAGATCATGATCAT 240
QY 307 CTTCTGAGCATCCAAATGTTCTTAGGATCAAAAGGAGCTTATGAAGATTCGGTGTGTT 366
Db 241 CTTCTGAGCATCCAAATGTTCTTAGGATCAAAAGGAGCTTATGAAGATTCGGTGTGTT 300
QY 367 CATATGTTATGAGGTTTGTGAAGTGTGAGCTTTTGTGCGATGTTCTTAAAGGT 426
Db 301 CATATGTTATGAGGTTTGTGAAGTGTGAGCTTTTGTGCGATGTTCTTAAAGGT 360
QY 427 CATTTTGTAGTGTGAGCTGTGAAGCTTATTAAGACGATTTCTTGGTGTGTTGAGGCT 486
Db 361 CATTTTGTAGTGTGAGCTGTGAAGCTTATTAAGACGATTTCTTGGTGTGTTGAGGCT 420
QY 487 TGTCTATCTCTTGGTGTATGATAGATGATCTCAACCTGAGAAATTTCTTGTGTATGT 546
Db 421 TGTCTATCTCTTGGTGTATGATAGATGATCTCAACCTGAGAAATTTCTTGTGTATGT 480
QY 547 CCTAAGATGATCTTAAGCTTAAGCTACCGATTTTGGTGTGTTGCTCTCTTATAGCCA 606
Db 481 CCTAAGATGATCTTAAGCTTAAGCTACCGATTTTGGTGTGTTGCTCTCTTATAGCCA 540
QY 607 GGCAATATTTATGACGTAGTGTGAAGTCCGTACTATGTTGCACGAGGTGCTTAAAG 666
Db 541 GGCAATATTTATGACGTAGTGTGAAGTCCGTACTATGTTGCACGAGGTGCTTAAAG 600
QY 667 AAATGTTATGGACCTGAATATGATGTGTGAGGTGCTGTTTATCTCTACATTTTACTC 726
Db 601 AAATGTTATGGACCTGAATATGATGTGTGAGGTGCTGTTTATCTCTACATTTTACTC 660
QY 727 AGCGTGTCTCTCCCTTCTGGGAGAGATGAGTCTGGAATCTTTAGACAGATTTGCCA 786
Db 661 AGCGTGTCTCTCCCTTCTGGGAGAGATGAGTCTGGAATCTTTAGACAGATTTGCCA 720
QY 787 GGAAGTTAGATTTCAATCTGACCGCTGGCTTACTATCTCAGAAAGTGTCTAAAGATTG 846
Db 721 GGAAGTTAGATTTCAATCTGACCGCTGGCTTACTATCTCAGAAAGTGTCTAAAGATTG 780
QY 847 ATCTATTAATGCTCGAAGAGGCCCCAAGAAGCGATTTCTGCTATGAGCTCTGTGT 906
Db 781 ATCTATTAATGCTCGAAGAGGCCCCAAGAAGCGATTTCTGCTATGAGCTCTGTGTGT 840
QY 907 CACCATGAGTGTGCTGATGAACAGCAGCACCAGACAGCTCTTGTATCAGCAGTCTTA 966
Db 841 CACCATGAGTGTGCTGATGAACAGCAGCACCAGACAGCTCTTGTATCAGCAGTCTTA 900
QY 967 TCTCGTCTAAGCAGTGTCTCAAAATGAATGAAGATTGAAGAAATGGCATTTACGGGTAA 1026
Db 901 TCTCGTCTAAGCAGTGTCTCAAAATGAATGAAGATTGAAGAAATGGCATTTACGGGTAA 960
QY 1027 GCTCAGAGACTTTTCAGAGGAGAAATTTGAGGTCTGAGGAATTTGTTCAAGATGATAGC 1086
Db 961 GCTCAGAGACTTTTCAGAGGAGAAATTTGAGGTCTGAGGAATTTGTTCAAGATGATAGC 1020
QY 1087 ACAGACAACAGCGGAGGATTTTCTGAAGAGTCAAAAGCGGTTTGAAGAGAGTCCGA 1146
Db 1021 ACAGACAACAGCGGAGGATTTTCTGAAGAGTCAAAAGCGGTTTGAAGAGAGTCCGA 1080
QY 1147 TCTGACTGTATGGAATCAGAAATCAAGTCTCTCATGATCGGCTGATATCGACAACAGT 1206
Db 1081 TCTGAACTGTATGGAATCAGAAATCAAGTCTCTCATGATCGGCTGATATCGACAACAGT 1140
QY 1207 GGTACAATAGACTACGGGAGATTTCTAGCAGCAACCTTTACACATCAACAAGATGAGAGA 1266
Db 1141 GGTACAATAGACTACGGGAGATTTCTAGCAGCAACCTTTACACATCAACAAGATGAGAGA 1200
QY 1267 GAGGAGATTTCTGGTGTGCTATTTTTCGAGCTTTGACAAGACGGAAGCGGTTATATCACC 1326
Db 1201 GAGGAGATTTCTGGTGTGCTATTTTTCGAGCTTTGACAAGACGGAAGCGGTTATATCACC 1260

QY 1327 ATCGATGAGCTTCAGTCTGACAGATTTGCTCTATGTGATACACCTCTGACGAC 1386
Db 1261 ATCGATGAGCTTCAGTCTGACAGATTTGCTCTATGTGATACACCTCTGACGAC 1320
QY 1387 ATGATCAAGGAGATTCATCTTGACAAATGACGGGAAGATCGATTCTCGAGTTTACAGCA 1446
Db 1321 ATGATCAAGGAGATTCATCTTGACAAATGACGGGAAGATCGATTCTCGAGTTTACAGCA 1380
QY 1447 ATGATGAGAAAGAGATGGAGTTGGGAGAGACAGAACCATGATGAAGAACTTGAACCTTC 1506
Db 1381 ATGATGAGAAAGAGATGGAGTTGGGAGAGACAGAACCATGATGAAGAACTTGAACCTTC 1440
QY 1507 AACATGCTGATGCTTTTGGAGTTGATGCTGAAGAAATCTGATGACTGA 1554
Db 1441 AACATGCTGATGCTTTTGGAGTTGATGCTGAAGAAATCTGATGACTGA 1488

RESULT 2

US-09-938-842A-786
; Sequence 786, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPT1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 786
; LENGTH: 1473
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-786

Query Match 42.6%; Score 744.2; DB 9; Length 1473;
Best Local Similarity 70.0%; Pred. No. 8.6e-173;
Matches 1001; Conservative 0; Mismatches 428; Indels 0; Gaps 0;

QY 106 GTTCTACCATATCAACACACCACGATTAAGAGATCAATACCTTCTGGGAAAAAGCTAGGC 165
Db 28 GTTCTTCTTACAGACCACAAAGGTTGAAGACAATTTACTTTCTTGGTCAAGTCTTGGA 87
QY 166 CAAGGCCAATTTGGAACAACCTATCTCTGCACAGAGAAATCAACCTCCGCTAATTAGGCC 225
Db 88 CAAGGCCAATTTGGAACAACCTATCTCTGTACCCATTAACACAGACAGGTCAAAAGCTTGGC 147
QY 226 TGCAAATCGATCCGAGCGAAAGCTGCTGTGCGGAGGATTAACGAGATGTATGCGGT 285
Db 148 TGCAAATCGATCCGAGCGAAAGCTGCTGTGCGGAGGATTAACGAGATGTATGCGGT 207
QY 286 GAGATTCAGATCATCATCTCTCTGAGCATCCAAATGTTTGTAGGATCAAGAGGACT 345
Db 208 GAGATTCAGATCATCATCTCTCTGAGCATCCAAATGTTTGTAGGATCAAGAGGACT 267
QY 346 TATGAAGATTCGGTGTGTTTTCATATTTGTTATGAGGTTTGTGAGGTTTGTGAGCTTTT 405
Db 268 TACGAGGACACAAAACGTCATCTTGTGATGAGGTTTGTGAGGAGGTGAGTGTGTT 327
QY 406 GATCGGATTTCTTAAGGTCATTTTAGTGAGGTCGAAGCTGCAAGCTTATTAAAGACG 465
Db 328 GATGAAGTTGTAAGAGAGGTCATTTACAGTGAAGAGAGAGCTGCTAGCTTATCAAGACC 387
QY 466 ATTCTTGTGTTGTTGAGGCTTGTCTCTTGTGTTGATGATGAGATCTCAACACT 525

Db 388 ATGTGGGTTGTGAGCGGTGTCACCTCTTGTTGTTGTCATAGAGATCTTAAGCCT 447
QY 526 GAGAAATTCCTGTTGATGCTTAAAGATGATGCTTAAGCTTAAAGCTACCGATTTGCT 585
Db 448 GAGAAATTCCTGTTGATGCTTAAAGATGATGCTTAAAGCTTAAAGCTACCGATTTGCT 507
QY 586 TTGCTGCTCTCTTAAGCAGGACAAATATATATGAGCTAGTTGGAAGTCCGCTACTAT 645
Db 508 CTCTCTGTTTCTGACACCGAGGAGCAATTTTCGAACTCGTTGGTGGTCTTACTAT 567
QY 646 GTTGACACAGGCTCTAAAGAAATGTTATGACCTGAAATAGATGTTGGAGTCTGCT 705
Db 568 GTGCACTGAGTTTACATAAGCATATGCTCTGATGCTGAGCTATGAGTCTGGA 627
QY 706 GTTATCCTCTACATTTTACTCAGCGGTGTTCCCTCTCTGCGCAGAGACTGAGTCTGGA 765
Db 628 GTTATCCTCTACATTTTACTCAGCGGTGTTCCCTCTCTGCGCAGAGACTGAGTCTGGA 687
QY 766 ATCTTTAGACAGATTCGAAGGAGTTAGATTTCAATCTGACCTGACCTGAGTCTACTAT 825
Db 688 ATCTTTAGACAGATTCGAAGGAGTTAGATTTCAATCTGACCTGACCTGAGTCTACTAT 747
QY 826 TCAGAAGCTCTAAGATTTGATCTATAAATGCTCGAAAGGAGCCCAAGAAAGCGCAT 885
Db 748 TCAGAAGCTCTAAGATTTGATCTATAAATGCTCGAAAGGAGCCCAAGAAAGCGCAT 807
QY 886 TCTGCTCATGAGCCTTGTGTCACCATGATGCTGATGATGATGATGATGATGATGAT 945
Db 808 ACTGCTCATGAGCCTTGTGTCACCATGATGCTGATGATGATGATGATGATGATGAT 867
QY 946 CCTCTTGATCCAGAGCTTATGCTGCTAAAGCAGTTTCTCAATGAATGAATGAATGA 1005
Db 868 CCTTTGACTCGCGGTAGTGTCCGCTGAGAGTTTCTGCAATGAATGAATGAATGA 927
QY 1006 AAAATGGCATTCGCGGTAAATGCTGAGAGCTTTTCAAGAGGAAATGAGGCTGAG 1065
Db 928 AAGATGGCTTTACGAGTATTCGAGAGAGCTATCTGAGGAGAAATCGGTGCTCAA 987
QY 1066 GAATTTGTTCAAGATGATGACACAGACAGACGAGAGCTATCTTTGAGAGCTCAA 1125
Db 988 GAATTTGTTCAAGATGATGACACAGATGATGAGGAGTATCTGAGTATGAGAGTTAAA 1047
QY 1126 GCGGTTTGAAGAGAGCTGATGCTGATGATGATGATGATGATGATGATGATGAT 1185
Db 1048 GATAGTATGAGAGCTTTGAGTACAGCTTATGATGATGATGATGATGATGATGAT 1107
QY 1186 GCGCTGATATGACAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1245
Db 1108 GCGCTGATATGAGAGCTTTGAGTACAGCTTATGATGATGATGATGATGATGAT 1167
QY 1246 CACATGAACAGATGAGAGAGAGATGCTGATGATGATGATGATGATGATGATGAT 1305
Db 1168 CACTTGACAGCTTGAAGAGTGAACAAATGATGATGATGATGATGATGATGATGAT 1227
QY 1306 GAGGAGAGCTTATATPACCATGATGATGATGATGATGATGATGATGATGATGAT 1365
Db 1228 GATGCAAGTGTATACATCACTATCGAAGAGCTTCAACAGGATGGAAGAGTTGGTATA 1287
QY 1366 TGTGATACACTCTGAGAGAGATGATCAAGAGATGATGATGATGATGATGATGATGAT 1425
Db 1288 AAGCATTTCTATCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1347
QY 1426 GATTTCTCGAGTTTACAGCAATGATGAGGAGGATGATGATGATGATGATGATGATGAT 1485
Db 1348 GACTATGGAATTTTGGCAATGATGAGGAGGATGATGATGATGATGATGATGATGAT 1407
QY 1486 ATGATGAAGACTTGACTTCAACATGCTGATGCTTTTGGAGTTGAT 1534
Db 1408 CGGAGAACTATGAGGACTCTCTACCTTTGGACTACTCTCTCTCTCTCTCTCTCTCT 1456

RESULT 3

US-09-938-842A-2344
; Sequence 2344, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAININ
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 2344
; LENGTH: 1635
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2344

Query Match 40.8%; Score 712.6; DB 9; Length 1635;
Best Local Similarity 68.3%; Pred. No. 5.3e-165;
Matches 988; Conservative 0; Mismatches 459; Indels 0; Gaps 0;

QY 73 ACAGAGCAAAACCCCTAGACGCTCTTCAACACAGTTCACCATATCAAAACACCAAGATTA 132
Db 184 ATGGCGGTAAAGTGTGACATCAATCTTACTATGTTCTTGTGTCACAAAGACTCTTAACAT 243
QY 133 AGAGATCATTAACCTCTGCGGAAAAGAGCTAGCCAGCCAAATTTGGACACCACTATCTC 192
Db 244 CCGTATCTTTACAGCTGTAGTCGTAAGTTAGGACAAAGACAAATTCGGGACCAAGTATTTG 303
QY 193 TGCACAGAGAAATCAACCTCCGCTAAATATACGCTGCAAAATCGATCCCGAGCAAGATC 252
Db 304 TGTACTGATATTCACAGAGGTGTGACTATGCTTGTAGTCTATATCAAGAGAAATG 363
QY 253 GTGTGTCGCGAGGATTCAGAGATGATGCGGTGAGATTCAGATTCAGATTCATCTCTCT 312
Db 364 ATATCTAAAGAGATGTTAGGATGTTAGGAGGAGATTCAGATTCAGATTCATCTAGCT 423
QY 313 GAGCATCCAAATGTTGTAGGATCAAGAGGACTTATGAAGATTCGTTGTTGTTGTTGTT 372
Db 424 GGTCAAGAAATATGTTACTATTAAGAGGACTTATGAGGATCCTTTGTTGTTGTTGTT 483
QY 373 GTATGAGGTTTGTGAAGTGTGAGCTTTTTCGATCGGATTTTTCGATCGGATTTTTCGAT 432
Db 484 GTGATGAGGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 603
QY 433 AGTGAAGCTGAAGCTGTCACACTTATTAAGAGATTCCTTGAAGATTCCTTGAAGATTC 492
Db 544 AGCGAGGAGAGGCTGCTGAGTTGACCAAGATCAATTCGCTGCTGCTGCTGCTGCTGCT 543
QY 493 TCTCTGCTGTTATGATAGATCTCAAACTGAGAAATTCCTTGTGTTGTTGTTGTTGTTGTT 552
Db 604 TCCTTGTGCTTATGATAGATTTTAAAGCTTGAAGATTTTCTTGTGTTGTTGTTGTTGTT 663
QY 553 GATGATGCTTAAGCTTAAGCTTACCGATTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTT 612
Db 664 GATGATTTCTCTCTTAAGGCAATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 723
QY 613 TATTTATACCTAGTGTGAAGTCCGATCTATGTTGACCAAGAGGCTGCTTAAAGAAATGT 672
Db 724 ATATCAAGGATGTTTGGAGTCCATATGTTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 783
QY 673 TATGGAGCTGAATAGATGTTGAGTGTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 732
Db 784 TATGGTCCAGAACTGATGTTGAGTGTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 843

QY	733	GI	T	C	C	T	C	C	T	T	C	T	G	G	C	A	G	A	C	T	G	A	G	T	C	T	T	T	A	G	A	C	A	G	A	T	T	C	C	A	G	G	A	G	792						
Db	844	G	T	C	C	C	C	T	T	C	T	G	G	C	A	A	A	C	A	C	A	G	A	A	T	A	T	T	G	A	T	T	G	A	T	T	G	A	G	G	A	T	903								
QY	793	T	T	A	G	A	T	T	C	A	A	T	C	T	C	A	C	C	G	T	G	G	O	C	T	A	C	T	A	C	T	C	A	G	A	G	T	G	T	A	A	G	A	T	T	T	C	A	T	852	
Db	904	A	T	T	G	A	C	T	T	G	A	C	A	C	C	G	T	G	C	T	G	C	A	T	C	C	G	A	C	G	T	A	A	G	A	T	C	T	A	A	G	A	T	C	G	963					
QY	853	A	A	A	T	G	C	T	C	G	A	A	G	A	G	C	C	C	A	A	A	G	C	A	T	T	C	T	G	C	A	T	A	A	G	A	G	O	T	T	G	T	G	T	C	A	O	C	C	A	912
Db	964	A	A	G	A	T	T	A	T	A	G	T	C	T	A	G	T	C	T	C	T	A	G	A	G	T	T	G	A	C	T	A	G	A	G	T	A	A	G	T	C	A	G	A	T	1023					
QY	913	T	G	A	T	T	G	A	T	G	A	A	C	A	C	A	G	C	C	T	C	T	T	G	A	T	C	C	A	G	A	G	T	C	T	T	A	T	C	T	C	G	T	972							
Db	1024	T	G	A	C	T	G	T	G	A	T	G	A	G	T	T	G	C	C	G	A	T	A	G	A	C	A	T	T	G	A	C	C	T	T	A	C	C	G	G	C	T	T	T	C	T	C	G	T	1083	
QY	973	C	T	A	A	A	C	A	G	T	T	T	C	C	A	A	T	A	A	T	A	A	G	A	T	T	A	A	A	A	T	A	A	A	T	A	A	T	A	A	T	A	A	T	T	C	T	G	A	1032	
Db	1084	C	T	A	A	A	C	A	G	T	T	T	C	T	C	A	A	T	A	A	T	A	A	A	G	A	T	T	A	A																					

RESULT 4

US-09-938-842A-2334
 ; Sequence 2334, Application US/09938842A
 ; Patent No. US20020160378A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Harper, Jeff
 ; APPLICANT: Kreps, Joel
 ; APPLICANT: Wang, Xun
 ; APPLICANT: Zhu, Tong
 ; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
 ; TITLE OF INVENTION: SAME, AND METHODS OF USE
 ; FILE REFERENCE: SCRIPI300-3
 ; CURRENT APPLICATION NUMBER: US/09/938, 842A
 ; CURRENT FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: US 60/227,866

Db 1185 AAGGTTAACTGCCACCAAGTAATATGTCATCCATGGTTCAAGTCGACGGTGTGGCTCC 1244
QY 939 AGAAGAGCCCTTGTATCCAGCAGTCTTATCPCGTCTAAGCAGTTTCTCAAAATGAATAA 998
Db 1245 AGAAGAGCCCTTGTATCCAGCAGTCTTATCPCGTCTAAGCAGTTTCTCAAAATGAATAA 1304
QY 999 GATTAAAGAAATGGCATACCGGTAATTCGTAGAGACTTTCAGAGGAAGAAATGGAGG 1058
Db 1305 GTTCAAGAAATGGCTTTAGAGTCAATTCGTAGAGCTTATCTGAAGAAATTCGCGGG 1364
QY 1059 TCTGAAGAAATGTTCAAGATGATAGACACAGACAGCGGGAACGATTACTTTTGAAGA 1118
Db 1365 CTGGAAGAAATGTTTAAATATGATAGATGCGGACAGAGTGGTCAAGATAACTTTCAAGA 1424
QY 1119 GCTCAAGAGCGGTTTGAAGAGTGGATCTGACTGATGGAATCAAGAAATCAAGTCTCT 1178
Db 1425 ACTCAAGAGCAGGACTAAACAGGTAGGGGCGAATCTCAAGAGGCTGAAATTCFCGACT 1484
QY 1179 CATGGATCGCGCTGATATCGACACAGTGGTACAAATAGACTACGGGAATTCCTAGCAGC 1238
Db 1485 GATCGAAGCTGCTGATGCGACACACCGGACAAATAGATACAAAGATTATAGCTGC 1544
QY 1239 AACCTTACATGAACAAAGATGAGAGAGAGGAGATTCTGGTGGCTGCATTTTCGGACTT 1298
Db 1545 AACATTACATCTAAACAAATAGAGAGAGAGGAGGACCATTTGTTTCGAGCTTTACATACTT 1604
QY 1299 TGCAAGAGCGGAGCGGTTATATCACCATCGATGAGCTTCAGTCACTTCGACAGATT 1358
Db 1605 TGCAAGAGCGGAGCGGCTTATATCACCCAGAGAGGCTTCAACAGAGTTGTGAGGAGTT 1664
QY 1359 TGGTCTATGTATACACCTCTGGACGACATGATCAAGAGAGATTGATCTTGACAAATGACGG 1418
Db 1665 TGGTGTGAGGATGTCGACATAGAGAACTGATCGCGGATGTTGATCAAGAAATGACGG 1724
QY 1419 GAAGATCGATTTCTCGGAGTTTACAGCAATGATGAGGAAAGAGAGTGGAGTGGGAGAAG 1478
Db 1725 GCGAATAGACTCAACAGAGTTTGTGGCGATGATGCGAAGAGGAGCATCACAGGAGACC 1784
QY 1479 CAGAACCATGATGAAGAACTTGAACCTTCAACATTGCT 1515
Db 1785 TGTGAATGGGCTAGAGAAAGCTTTAGCAATGCT 1821

RESULT 5

US-09-828-313-26
; Sequence 26, Application US/09828313
; Patent No. US20020059662A1
; GENERAL INFORMATION:
; APPLICANT: COSTA e SILVA, OSWALDO DA
; APPLICANT: BOHNERT, HANS J.
; APPLICANT: THIELEN, NOCHA VAN
; APPLICANT: CHEN, ROUYING
; APPLICANT: SARRIA-MILLAN, RODRIGO
; TITLE OF INVENTION: PROTEIN KINASE STRESS-RELATED PROTEINS AND METHODS OF
; TITLE OF INVENTION: USE IN PLANTS
; FILE REFERENCE: 16313-0032
; CURRENT APPLICATION NUMBER: US/09/828,313
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/196,001
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 26
; LENGTH: 2230
; TYPE: DNA
; ORGANISM: Physcomitrella patens
US-09-828-313-26

Query Match 30.4%; Score 531.8; DB 10; Length 2230;
Best Local Similarity 62.5%; Pred. No. 1.7e-120;
Matches 849; Conservative 0; Mismatches 507; Indels 3; Gaps 1;

QY 141 TTACTCTCTGGGAAAAAGCTAGCCCAAGGCCAAATTTTGAACAAACCTATCTCTGCACAGA 200
Db 602 TTACATCTCTGGGAGGAGCTTGGCCGAGGCGAGTTCGGAGTACTTACTTGTGTACTGA 661
QY 201 GAAATCAACCTCCCTAATACGCTTCAAAATCGATCCGAGAGGAAAGCTCGTGTGTGCG 260
Db 562 CAAGATGACGATGAGCGGTACGCGTCCAGAGATCGCCAAACGGAACCTGACCACTAA 721
QY 261 CGAGGATTACGAAGATGATGGCGTGAGATTTCAGATCATCATCTCTCTGAGCATCC 320
Db 722 GGAGGATATCGAGGATGTTAAGCGGAGGTTTCAGATTATGCATCACCCTGTCGGGACACC 781
QY 321 AAATGTTGTAGGATCAAGGAGCTTATGAAGATTTCGGTGTGTTTTCATATTTGTTATGGA 380
Db 782 CAATATCGTGGTGTAAAGGATGTTTCGAGGACAAAGCATTCCTGTCATCTTGTGATGA 841
QY 381 GGTGTTGAAGGTTGGTGGATTTTGTGATCGGATTTTCTAAAGGTCATTTTGTAGTGAGCG 440
Db 842 GCTCTGTGAGGTTGGCGAGCTCTTCGATCGCATCATTTGCCAAGGGGCAATTACAGTGAGCG 901
QY 441 TGAAGCTGTCAAGCTTATTAAGACGATTCTTGTGTTGTTGAGGCTTGTCTCTCTCTG 500
Db 902 CGCGCTGCGGATATGTCAGAGTCACTCAATGTGTCACAGATGCCACATCATTAGG 961
QY 501 TGTATGATAGAGATCTCAAACTGAGAAATTTCTTCTTTGATAGTCTCTAAAGATGATGC 560
Db 962 GGTCTTCATCGGATCTCAAGCCAGAGAAATTTCTTGTGCCAGCAAGGCTGAGGATGC 1021
QY 561 TAAAGCTTAAAGCTTACCGATTGTTGTTGCTCTCTCTATTAAGCCAGCAATAATTTATA 620
Db 1022 GCCTCTGAAGCCACAGACTCGGCTGTCAACTTTTAAAGCCAGGATGTGTCTCA 1081
QY 621 TGAGCTAGTTGGAAGTCCGTAATGTCAGAGAGTCTTAAAGAAATGTTATGAGACC 680
Db 1082 GGATATGTTGGAAGTCCGTAATGTCAGGTCGCTTGAAGTTTGAAGAGAGTTATGCTCC 1141
QY 681 TGAATAGATGTTGAGAGTCTGTTTATCTCTTACATTTTACTCAGCGGTTGTTCTCTC 740
Db 1142 TGAAGCTGATGTTGAGAGTCTGAGGCTGATGTTGTATCTCTGCTGTGTGTACCC 1201
QY 741 CTCTCTGGCAGAGACTGAGTCTGGAATCTTTAGACAGATATTCAAGGGGAGTTAGATT 800
Db 1202 CTCTCTGGCTGAACCTGACGAGGATCTTTGAGCTGTCTCAAGGGGACATAGACTT 1261
QY 801 CAAATCTGACCCCTGGCTTACTATCTCAGAGCTGCTTAAAGATTGATCTATATAATGCT 860
Db 1262 CGAGAAAGATCCATGCCGAAATCTCCAACGGGCTTAAGATTGTTGAGGAGAAATGCT 1321
QY 861 CGAAGAGGCCCCAAGAAAGCAATTTCTGTCATGAAGCCTTGTGTCAACCCATGGATTGT 920
Db 1322 AAACCTTAAAGTGAAGATAGCTGTGACGGCACAGCAGGTTTGAAGCATCCATGGATGA 1381
QY 921 CGATGAACAGCAGCAGCAGCAAGCTCTTGTATCAGCAGTCTTATCTCTGCTCAAGCA 980
Db 1382 GGAAGATGTTGATGCTCCAGACGCTGCCATCGACATCGGCTGTTACACAGACTGAAA 1441
QY 981 GTTTCTCAAAATGAATAGATTAAAGAAATGCAATTTACGGTAAATGCTGAGAGACTTTC 1040
Db 1442 TTTCTCAGCGCCCAACAAGATGAAAAAGTGGCGCTGAAGTTGTCAGAGAGTCTGTC 1501
QY 1041 AGAGGAAAGAAATGAGGCTCTGAAGAAATGTTCAAGATGATAGACACAGCAACAGCG 1100
Db 1502 GGAGGAAAGAGTCTGGGGTTGAGGAGATGTTCAATCCATAGATACAGCAACAGCGG 1561
QY 1101 AACGATTACTTTTGAAGAGCTCAAGCGGTTTGAAGAGAGTGGATCTGAAGTATGA 1160
Db 1562 CACGGTGAAGCTTCGAGAGCTTAAAGAGGTTTGTGAAGCAGGCTCAAACTAATGA 1621
QY 1161 ATCAGAAATCAAGTCTCTCATGATCGGCTGATATCGCAACAGTGTGATACATAGACTA 1220
Db 1622 ATCGGACATCAGAAACTAATGGAAGCTCAGATGTCGATGGAACGGCAAGATCGACTT 1681
QY 1221 CGGAGAAATTCCTAGCAGCAACCTTACATGTAACAGATGGAAGAGAGAGATTCTGTT 1280

Db 1682 CAACGAGTTCATATCGGCAACAATCCATGAACAAGACGGAGAAGAGGATCACCTTTG 1741
QY 1281 GCGTCATTTTCGGACTTTGACAAAGACGGAGCGGTTATATCAACATCGATGAGCTTCA 1340
Db 1742 GGCACATTCATGCAATTCGACACCGCAATAGCGGGTATATCACCATCGAGAGCTTCA 1801
QY 1341 CTCACATGTCACAGAGTTGGTCTTATGTATAC---ACCTCTGGACGACATGATCAAGAA 1397
Db 1802 GGAAGCAATCGGAAGAATGGAATGGAGATCCTGAGACACCTCCAAAGAGATCATCAGGGA 1861
QY 1398 GATTGATCTTGACATGACGGGAAGATCGATTCTCGGAGTTTACAGCAATGATGAGAA 1457
Db 1862 GTGACACACACACGACGGAGGAATAGACTACGACGAGTTCTGAGCCATGATCGGCA 1921
QY 1458 AGGAGATGAGTTGGGAGAGACAGAACCATGATGAAGAA 1496
Db 1922 GGGCAATCTCGCGCTGAAACCGGAGGAAACGGTGAACAA 1960

RESULT 6

US-09-938-842A-1859
; Sequence 1859, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1859
; LENGTH: 1638
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1859

Query Match 29.1%; Score 507.8; DB 9; Length 1638;
Best local similarity 61.7%; Pred. No. 1.1e-114;
Matches 828; Conservative 0; Mismatches 507; Indels 6; Gaps 1;

QY 131 TAAGAGATCATTAACCTCTCTGGAAAAAGCTAGGCCAAGCCCAATTTGGAAACAACCTATC 190
Db 176 TCAGCGCAAAATACATCTTAGTCGTGCAATTAGTCGAGCGGAATTCGGAAATCACATTAC 235
QY 191 TCTGCACAGAGAATCAACCTCCGCTAAATTAACGCTCAAAATCGATCCCGAAGCGAAAGC 250
Db 236 TCCTGACTGATGCTGTAACCCAGCAAGCTTAGCTTCAAAATCGATTTCAAGCGAAAGC 295
QY 251 TCGTGTCTCGGAGGATGACAGATGATGCGGTGAGATTCAGATCATCATCTCT 310
Db 296 TTCAACAGCTGTGATATGCAAGACCTTCGTCGTGAGGTAGCGATATGCTACTATTAC 355
QY 311 CTGAGCATCCAAATGTTGTAGGATCAAGAGGACTTATGAGATTCGGTGTTCCTTCATA 370
Db 356 CTGAGCATCCAAAGTATGAGCTTAAGCTTAGGCTAGTTATGAGGATTAACGAAACGTGATC 415
QY 371 TTGTTATGGAGTTTGTGAAGTGGCTGAGCTTTTGTATCGGATTTCTTAAAGGTCATT 430
Db 416 TGGTTATGGAGCTTTGTGAAGGAGGCTGAGCTTTTGTATCGGATTTCTTAAAGGTCATT 475
QY 431 TTAGTGACGCGAAGCTGTCAGCTTTATTAAGACGATCTTGGTGTGTTGAGGCTTGTC 490

Db 476 ACACGAGCGTGCTCTCGAGCTGTTGCGAGACAGATTGCTCAGGTTGTGATGATGTGC 535
QY 491 ATTCTCTTGGTGTATGATCATGAGATCTCAAACTCGAGAATTTCTTGTTGATGATCTCTA 550
Db 536 ACTCTAATGAGGTTATGATCATGAGATTTGAAAACCTCGAGAATTTCTTGTTGATGATGATA 595
QY 551 AAGATGATGCTTAAGCTTAAGGCTACCGATTGTTGGTTTCTGCTCTCTATAGCCAGGAC 610
Db 596 AGGAAATCTCCCACTAAAGGCTATTGATTGTTGGCTGTTCTGCTCTCTCAAACTCTGAG 655
QY 611 AATATTTATATGACCTAGTTGGAAGCTCGTACTATGTTGCCACAGAGTGTCTAAAGAAAT 670
Db 656 ATAACTTTACAGAGATTTAGGAAGTCCGTTATTAATGCTCCCAAGATGTTTGAAGAGAG 715
QY 671 GTTATGGACCTGAATATGATGTTGAGTGTGCTGTTGTTATCTCTACATTTTACTCAGCG 730
Db 716 ATTATGGACCGAGGTTGATGTTGAGTGTGCGGAGTTATTAATCTATATCTTCTGCTGTG 775
QY 731 GTGTTCTCTCTCTGCGCAGAGACTGAGTCTGGAATCTTTAGACAGATATTGCAAGGGA 790
Db 776 GTGTTCTCTCTCTGCGCTGAGACTGAACAGGTGTTGCTCTTGGATCTTTCGCGGAG 835
QY 791 AGTTAGATTTCAAACTGACCGTGGCTCTACTATCTCAGAACTGCTTAAGATTTGATCT 850
Db 836 TTCTTGATTTTAAGAGAGACCTTGGCTCTCAGATATCAGAGAGTGCCTCAAGAGCCTTGTGA 895
QY 851 ATAAATGCTCGAAAGGAGGCCCAAGAAAGCATTTCTCTCATGAAGCTTTGTGTCACC 910
Db 896 AGCAGATGTTGGATCTGATCGACTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 955
QY 911 CATGATGTTGATGAACAGAGCAGCAGCAGCAGCAGCTTGTGATCCAGCAGCTTATCTC 970
Db 956 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1015
QY 971 GTCTAAAGCAGTTTCTCAATGAATAAGATTAAGAAATGCGATTTACGGGTAATTTGCTG 1030
Db 1016 GGTGGAAGCAGTTCTCTATGATGACAGATTTCAAAAGAAAGTTCTCTGTTAAATTTGCGG 1075
QY 1031 AGAGACTTTTCAGAGGAGAAATTTGAGGTTCTGAAGAAATTTTCAAGATGATAGACACAG 1090
Db 1076 AGCATTGTTCTTCAAGAGTTGAGTGAATGAATGAATGAATGAATGAATGAATGAATGA 1135
QY 1091 ACAACAGCGGACGATTTACTTTTGAAGAGCTCAAGCGGTTTGAAGAGAGTGGGATCTG 1150
Db 1136 ACAAGGATGTTAAATAAATTAACCTTACCCGAACTCAAGCTGGCTTCAGAAAGTGGTTCAC 1195
QY 1151 AACTGATGGAATCAGAAATCAAGTCTCTCATGATGCGCTGATATCGACACAGTGTGA 1210
Db 1196 AACTGTTGAACAGAGATCAAAATGTTGATGAAGTGGCGGATGTCGATGGAAATGGGT 1255
QY 1211 CAATAGACTACGAGAGATTTCTAGCAGCAACCTTACACATGAACAGATGAGAGAGAGG 1270
Db 1256 TTCTGGATTTAGAGAGTTGTTAGCTGTGATAATTCATTTGCAAGAGATAGAGAAATGATG 1315
QY 1271 AGATTCGTGTTGGCTGCAATTTTCGACATTTTGAACAGAGAGAGAGAGAGAGAGAGAG 1330
Db 1316 AACTTTTCAACATGAGCTTTTATGTTTTCGACAAAGATGGAAGTACATACATTTGAACTTG 1375
QY 1331 ATGAGCTTCACTGAGCTTTCACAGA-----GTTTGTCTATCTGTATACACCTCTGGAGC 1384
Db 1376 ATGAGTACCGGAGCTTTTACCGGATGAGTTAGCGAGCCAGAGCCAGTGTCTAAGCG 1435
QY 1385 ACATGATCAAGGAGATTTGATCTTGACAATGACGGGAGATCGGATTTCTCGGAGTTTACAG 1444
Db 1436 ACATCATGCTGAGTTGACACTGACAGAGGAGCGGACCTATAAATATGATGAGTGTGTA 1495
QY 1445 CAATGATGAGGAAGGAGATG 1465
Db 1496 CGATGATGAAGCTGGAACGTG 1516

RESULT 7
US-09-770-444-571

; Sequence 571, Application US/09770444
; Patent No. US2002023280A1
; GENERAL INFORMATION:
; APPLICANT: Gorlach, Jorn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Kriker, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurlan, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE REFERENCE: 2027 (PARA-016PRV)
; CURRENT APPLICATION NUMBER: US/09770.444
; PRIOR FILING DATE: 2001-01-26
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 571
; LENGTH: 455
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(455)
; OTHER INFORMATION: n = A,T,C or G
US-09-770-444-571

Query Match 25.7%; Score 448.2; DB 10; Length 455;
Best Local Similarity 98.9%; Pred. No. 2.2e-100;
Matches 450; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 999 GATTAAAGAAATGCGATTACGGGTAAATGCTGAGAGACTTTTCAGAGGAAGAAATTTGGAGG 1058
Db 1 GATTAAAGAAATGCGATTACGGGTAAATGCTGAGAGACTTTTCAGAGGAAGAAATTTGGAGG 60
QY 1059 TCTGAAGGAATTTGTTCAAGATGATAGACACAGACAGCGGAGGAGGATTTTGTGAGA 1118
Db 61 TCTGAAGGAATTTGTTCAAGATGATAGACACAGACAGCGGAGGAGGATTTTGTGAGA 120
QY 1119 GCTCAAGCGGGTTTGAAGAGAGTCGGATCTGAACTGATGGAATCAGAAATCAAGTCTCT 1178
Db 121 GCTCAAGCGGGTTTGAAGAGAGTCGGATCTGAACTGATGGAATCAGAAATCAAGTCTCT 180
QY 1179 CATGGATGCGGCTGATATCGACACAGTGGTACAAATGACATACGGAATTCCTAGCAGC 1238
Db 181 CATGGATGCGGCTGATATCGACACAGTGGTACAAATGACATACGGAATTCCTAGCAGC 240
QY 1239 AACCTTACATGAACAAAGATGGAGAGAGGAGATTTCTGGTGGCTGCATTTTCGGACTT 1298
Db 241 AACCTTACATGAACAAAGATGGAGAGAGGAGAAATCTGGTGGCTGCATTTTCGGACTT 300
QY 1299 TGACAAAGACGGAAGCGGTTAATCACCATGATGAGCTTCAGTCAGCTTGCACAGAGTT 1358
Db 301 TGACAAAGACGGAAGCGGTTAATCACCATGATGAGCTTCAGTCAGCTTGCACAGAGTT 360
QY 1359 TGGTCTATGTGATACACTCTGGACGACATGATCAAGAGANTGATCTTGACAAATGACGG 1418
Db 361 TGGTCTATGTGATACACTCTGGACGACATGATCAANNAGATTGATCTTGACAAATGACGG 420

QY 1419 GAAGATCGATTTCCTCGGAGTTTACAGCAATGATGA 1453
|||||
Db 421 GAAGATCGATTTCCTCGGAGTTTACAGCAATGATGA 455
RESULT 8
US-09-938-842A-2304
; Sequence 2304, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAININ
; FILE REFERENCE: SCRIP1300-3
; CURRENT APPLICATION NUMBER: US/09/938.842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 2304
; LENGTH: 1602
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2304

Query Match 25.4%; Score 444.6; DB 9; Length 1602;
Best Local Similarity 59.7%; Pred. No. 3.6e-99;
Matches 788; Conservative 0; Mismatches 524; Indels 9; Gaps 2;

QY 142 TACCTTCGCGGAAAGAGCTAGGCCAAGCCAAATTTGGAACAACCTATCTCTGACACAGAG 201
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Db 159 TATGATCTGGGCGGTGAGGTTGGTCGGGAGAGTTGGTATTACTTACTTGTGCACTGAT 228
QY 202 AAATCAACCTCCGCTAAATTAGCCCTGCAAAATCGATCCGGAAGCAAGCTCGTGTGCGC 261
|||
Db 229 ATCAAAAGCGGCGAAGATGTCGTCGCAAGTCTATATCAAGAAGAGAGCTTAGAACAGCT 288
QY 262 GAGGATTACGAAGATGATGCGGTGAGATTCAGATCATCATGATCATCTCTGAGCATCCA 321
|||
Db 289 GTGATATAGAGGATGTTAGGAGGGAAGTTGAGATATGAACATATGCCATAGACACCCA 348
QY 322 AATGTTGTTAGGATCAAGGGAAGCTTATGAAGATTCGGTGTGTTTCATATTTGTTATGGAG 381
|||
Db 349 AATATCGTGTGCGTGAAGGATGCGCTTTGAGGATGATGATGATGATGATGATGATGATG 408
QY 382 GTTGTGAAAGGTGCTGAGCTTTTGTGCGGATTTGTTCTAAAGGTCAATTTTGTGAGCGT 441
|||
Db 409 TTGTTGAAAGGAGGTGAGCTGTTTGTGCGGATTTGCTAGAGCTCATTTACTAGAGCGA 468
QY 442 GAAGCTGCAAGCTTTAAGACGATTTCTTGGTGTGTTGAGGCTTGTCAATTTCTTTGGT 501
|||
Db 469 GCTGCTGTCAGTGAAGAGCTATTTCTGAAGTTGTCAGATATGCCATAGCAGATGGA 528
QY 502 GTTATGATAGAGATCTCAACCTGAGAAATTTCTGTTGATAGTCCCTAAGATGATGCT 561
|||
Db 529 GTGATGATCGGATCTAAAGCCCTGAGAACTTTCTCTTCTGCAATAAAGAGACATCA 588
QY 562 AAGCTTAAGGTACCGATTTTGGTTTCTGCTCTCTATAGCCAGGACACATATTTATAT 621
|||
Db 589 GCCCTTAAGCCATAGATTTTGGATTAATCAGTCTTCTCAAGCCGTGGTGAAGATTCAC 648
QY 622 GACGTAGTTGGAAGTCGCTACTATGTTGACCCAGAGAGTGTAAAGAAATTTTATGGACCT 681
|||
Db 649 GAGATTGTTGAAGTCTCTTATTACATGGCAGGAGTACTTAGCCGAAATACGGACCT 708
QY 682 GAAATAGATGTGGAGTGTGGTGTGTTATCTCTACATTTTACTCAGCGGTTCCTCC 741

Db	709	GAGGTTGATATCTGAGTGCCTGGAGTTATCCTTTATATCCTGCTGTGGTGCTGCCACCA	768
QY	742	TTCTGGCCAGACGTCTGGAATCTTTAGACAGATATTGCAAGGAAGTTAGATTTC	801
Db	769	TTTGTGGCCGACGTGACGAAGGGTGGCTCAGCGCATTAITAGTCAGTTAICGACTTT	828
QY	802	AAATCTGACCCGTGGCTACTACTCTCAGAAGCTCTAAAGATTTGATCTATAAATGCTC	861
Db	829	ARAGAGGATCCATGCCCGAGAGTTCTGAGACTGCCAAGACCTTTGTGAGGAAGATGCTC	888
QY	862	GAAGAGGCCCCAAGAACGCAATTTCTGCTCATGACGCCITGTGTCAACCATGGATTGTC	921
Db	889	GAACCTTGACCCCAAAAACGGCTTCTGCTCCACAAGTACTCGAACAATCTTGGATTACAA	948
QY	922	GATGACAAAGCAGCACAGACAGCTCTTCATCCAGCAGTCTTATCCTCTCTAAAGCAG	981
Db	949	AATGGAGAAAGGCTCCAAATGTTTCTCGCGGAGACGGTGAAGCAAGACTCAAAAG	1008
QY	982	TTTTCTCAATGAATAAGATTAAAGAAAATGGCATACGGSTAAITGCTGAGAGACTTCA	1041
Db	1009	TTTTCTGTTATGAACAAGCTCAAGAAAGAGCGCTACGGSTGATAGCGGAACACTTATCA	1068
QY	1042	GAGGAGAAATTTGGAGGCTCTGAAGGAATGTTCTAAGATGATAGACACAGACACGCGGA	1101
Db	1069	GTGGAGGAAGTAGCTGGCATCAAGGAAGCAITTTGAGATGATGGACAGTAAAAAGACGGGA	1128
QY	1102	ACGATTACTTTCAAGAGCTCAAGCGGTTTTGAAGCAGTTCGATCTGAACATGAT--G	1158
Db	1129	AGAATAACCTCGAGAGCTTAAATTTGACTTCATAACTCGGACAGCAGATACCT	1188
QY	1159	GAATCAGAAATCAAGTCTCTCATGGATCGGCTGATATCGACAACAGTGTCAAAATAGAC	1218
Db	1189	GATACTGATCTACAGATTCTGATGGAAGCTGCTGATGTTGATGGGATGGGACTTTAAAT	1248
QY	1219	TACGGAGAATTCCTAGCAGCAACCTTACACATGACACAGATGGAGACAGAGGAGATPCTG	1278
Db	1249	TATGGGCAGTTTGTGGTGCTCTGTGTGCATCTTAAGAAAAATGGCGACGCAACACTTG	1308
QY	1279	GTGGCTGCATTTTCGAGACTTTGACAAAGACGGAAGCGGTTATATCAACCATCGATGACITT	1338
Db	1309	CATAAGGCTTTTASCTTTTTCGACCAAGATCAGACGGATACATAGAGATTGAGGAGCTG	1368
QY	1339	CAGTCAGCTTGACAGA-----GTTTGGTCTATGTGATACACCTCTCGGACGACATGATC	1392
Db	1369	CGTGAGGCTTTAAATGATGAGGTGGATACTACAGTGAAGAAATGTTTGCAGCTATTATG	1428
QY	1393	AAGGAGATTGATCTTGACAAATGACGGGAAGATCGATTCTTCGGAGTTTTCACGAACATGATG	1452
Db	1429	CAAGATGTCACAGACAGAAGGACGCGCAAGTAAGCTATGAAGAGTTTTCGGCGCATGATG	1488
QY	1453	A 1453	
Db	1489	A 1489	

RESULT 9

US-09-988-462-20
; Sequence 20, Application US/09988462
; Publication No. US20030046726A1

GENERAL APPLICANT:	Koztel, Michael G.
INVENTOR:	Desai, Nalini M.
	Lewis, Kelly S.
	Kramer, Vance C.
	Warten, Gregory W.
	Evola, Stephen V.
	Crossland, Lyle D.
	Wright, Martha S.
	Merlin, Ellis J.
	Launis, Karen L.
TITLE OF INVENTION:	SYNTHETIC INSECTICIDE

NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: Syngenta Biotechnology, Inc.
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/988,462
FILING DATE: 20-NO. US20030046726A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/547,422
FILING DATE: 11-APR-2000
APPLICATION NUMBER: US 08/459,504
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-188051
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 1349 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 3..1226
OTHER INFORMATION: /note= "cDNA sequence for maize
pollen-specific calcium dependent protein kinase gene as
disclosed in Figure 30."
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-988-462-20

Launius, Karen L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
SYNTHETIC ACTIVITY IN MAIZE

QY	590	CTGCTCTTCTAAGCCAGGCAATATTTATATGACGTAGTTGGAGTCCGTACTATGTTG	649	APPLICANT: THIELEN, NOCHA VAN
Db	301	CGGTCTTCTTCAAGGAGGCGAGCGTCCTCAGGACATCGTCGGCAGCGCCCTACTACATCG	360	APPLICANT: CHEN, ROUYING
QY	650	CACAGAGTGTAAAGAAATTTATGGACCTGAAATAGATGTGTGGAGTGTGTTGTTGTA	709	APPLICANT: SARRIA-MILLAN, RODRIGO
Db	361	CGCCGAGGTCTCAAGAGGAAGTACGCGCCGAGGCGGACATCTGGAGCGTCGCGCTCA	420	TITLE OF INVENTION: PROTEIN KINASE STRESS-RELATED PROTEINS AND METHODS OF
QY	710	TCTCTACATTTTACTACGCGTGTTCCTTCTTGGCAGAGACTGAGTCTGGAATCT	769	TITLE OF INVENTION: USE IN PLANTS
Db	421	TGCTCTACATCTTCTCGCGCGGTCTCTCTTCTGGCAGAGCAACGAGACGGCATCT	480	FILE REFERENCE: 16313-0032
QY	770	TTAGACAGATATTCAGAGGAGTGTAGATTTCAAAATCTGACCCGTGGCTACTATCTCAG	829	CURRENT APPLICATION NUMBER: US/09/828,313
Db	481	TCACGCCATCTCGGAGGCGAGCTTGACCTCTCCAGCGAGCATGGCCACACATCTCGC	540	CURRENT FILING DATE: 2001-04-06
QY	830	AAAGCTCTAAAGATTGATCTATAAATGCTGAAAGAGCCGCCAAGAAACGCAATTTCTG	889	PRIOR APPLICATION NUMBER: 60/196,001
Db	541	CGGAGCCAGGATCTCGTCAGAGAGTCTCAACATCAACCCCAAGGAGCGGCTCACGG	600	PRIOR FILING DATE: 2000-04-07
QY	890	CTCATGAAGCCTTGCTCCACCCGATGATGTCGATGAACAAGCAGCACCAGACAACCTTC	949	NUMBER OF SEQ ID NOS: 128
Db	601	CGTTCAGGTCTCTCAATCAACCCATGATCAAAAGAACGAGCAGCGGCTGACACCGCGC	660	SOFTWARE: PatentIn Ver. 2.1
QY	950	ITGATCCAGCAGTCTTATCTCGTCTAAAGCAGTTTTCTCAATGGAATAAGATTAAAGAAA	1009	SEQ ID NO 13
Db	661	TTGACAAAGTGTCTGACAGGCTCAAGCAGTTCAGGCGCAATGACCCAGTCAAGAAAG	720	LENGTH: 1387
QY	1010	TGGCATTACGGGTAATTTGTGAGAGCTTTTACAGGAAGAAATTTGAGGTCCTGAAGGAT	1069	TYPE: DNA
Db	721	CAGCATTGAGGATCATAGCTGGGTGGCTATCCGAAGAGGAGATCAAGGGCTGAAGGAGA	780	ORGANISM: Physcomitrella patens
QY	1070	TGTTCAAGATGATAGACACAGACAGCGGAAAGTACTTTTGAAGAGCTCAAGCGG	1129	FEATURE:
Db	781	TGTTCAAGACATTTGACAGAGGATAACAGCGGACCATTTACCTCGACAGCTCAACACG	840	NAME/KEY: modified_base
QY	1130	GTTTGAAGAGAGTGGATCTGAAGTGAATGGAATCAAGTCTCTCATGATCGCG	1189	LOCATION: (1385)
Db	841	GGTTGGCAAGCAGCGGCCCAAGCTGTACAGACGCGAAATGGGAAACTAATGGAGCAG	900	OTHER INFORMATION: a, t, c, g, other or unknown
QY	1190	CTGATATCGACACAGTGGTACAAATAGCTACGAGATTCCTAGCAGCAACCTTACACA	1249	US-09-828-313-13
Db	901	CTGACGTGACGCAACCGGTTAATGACTACGACGAAATTCGTCAACGCAACATTCGATA	960	Query Match 15.9%; Score 277.8; DB 10; Length 1387;
QY	1250	TGAACAAGATGAGAGAGGAGATTCCTGFGGCTGCAATTTTGGACTTTTGACAAAGACG	1309	Best Local Similarity 63.4%; Pred. No. 3.1e-58;
Db	961	TGAACAACACTGGATAGAGAGACACCTTTTACACAGCATTCAGTATTTGACAAAGACA	1020	Matches 457; Conservative 0; Mismatches 262; Indels 2; Gaps 2;
QY	1310	GAAAGGTTATPATCACCATCATGAGCTTCAGTTCAGTTCAGAGATTTGGTCTATGTG	1369	
Db	1021	ACAGCGGTACTACTAAAGAAGAGCTTGACGCGCTTGAAGGCAAGGGTGTATG	1080	
QY	1370	ATACACCT--CTGACACATGATCAAGGAGATTGATCTTGACAAATGACGCGAAGATCG	1426	
Db	1081	ACGCGATAAATCAAGACATCATCTCCGATGCCACCTCTGACATCTGACATGATGAAGTAG	1140	
QY	1427	ATTTCTCGAGTTTACACCAATGATGAGGAAAGAGATGGATTTGGGAGAGCAGAAACA	1486	
Db	1141	ATTATTCAGATTTCTGGCGATGATGAGGAAAGGACGGCTGGTCCCGCGCAATGAACA	1200	
QY	1487	TGATGAAGA 1495		
Db	1201	TCAAGAAGA 1209		
RESULT 10				
US-09-828-313-13				
Sequence 13, Application US/09828313				
Patent No. US2002059662A1				
GENERAL INFORMATION:				
APPLICANT: COSTA e SILVA, OSWALDO DA				
BOHNERT, HANS J.				

ORGANISM: Arabidopsis thaliana
US-09-938-842A-1063
Query Match 11.5%; Score 200.6; DB 9; Length 1800;
Best Local Similarity 52.4%; Pred. No. 3.4e-39;
Matches 490; Conservative 0; Mismatches 439; Indels 6; Gaps 2;
229 AATCGATCCCGAAGGCTCGTGTGCGAGGATTACGAAAGATGTAAGGCTGAG 288
DB AATCGATCCCGAAGGCTCGTGTGCGAGGATTACGAAAGATGTAAGGCTGAG 585
289 ATTGAGATCATCATCTCTCTGAGCATCCAAATGTTGTTAGGATCAAGGCTTAT 348
DB ATTGAGATCATCATCTCTCTGAGCATCCAAATGTTGTTAGGATCAAGGCTTAT 585
586 GTGAAATACCTCGGCGCTTATCTGACATCAAAATTTGTTACAAATTTCTATGCGTTC 645
DB GTGAAATACCTCGGCGCTTATCTGACATCAAAATTTGTTACAAATTTCTATGCGTTC 645
349 GAAGATTCGGTGTGTTTCTCATATTGTTTGAAGGTTGTTGAAGGTTGTTGTTGAT 408
DB GAAGATTCGGTGTGTTTCTCATATTGTTTGAAGGTTGTTGAAGGTTGTTGTTGAT 705
646 GAGGACAATGCCAAGCTTTACATCGTTATGAGGATGTTGAGGAGGTTGTTGAT 465
DB GAGGACAATGCCAAGCTTTACATCGTTATGAGGATGTTGAGGAGGTTGTTGAT 705
409 CGGATGTTTCTA--AAGTCTATTTAGTGAGCGTGAAGCTGTCAAGCTTTAAGACG 465
DB CGGATGTTTCTA--AAGTCTATTTAGTGAGCGTGAAGCTGTCAAGCTTTAAGACG 765
706 AGGATCTAGCAAGGAGGAAATCTCTGAAGATGATCAAAAGCAGTGTCTTATACAG 525
DB AGGATCTAGCAAGGAGGAAATCTCTGAAGATGATCAAAAGCAGTGTCTTATACAG 525
466 ATTCCTTGGTGTGTTGAGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 825
DB ATTCCTTGGTGTGTTGAGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 825
766 ATCCCTTAACGTCGTAGCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 585
DB ATCCCTTAACGTCGTAGCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 885
526 GAGAAATCTCTGTTGATAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 645
DB GAGAAATCTCTGTTGATAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 885
826 GAGAAATCTCTGTTGATAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 945
DB GAGAAATCTCTGTTGATAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 945
586 TTGCT 705
DB TTGCT 705
886 TTATCGGACTTTGTCAGACCCAGCAAGAACTAAATGATATAGTGGGAAGTGCATAT 1005
DB TTATCGGACTTTGTCAGACCCAGCAAGAACTAAATGATATAGTGGGAAGTGCATAT 1005
646 GTTGCCACCAAGGCT 765
DB GTTGCCACCAAGGCT 765
946 GTACCCCT 1065
DB GTACCCCT 1065
706 GTTATCT 825
DB GTTATCT 825
1006 GTCATAGCATATCT 1125
DB GTCATAGCATATCT 1125
766 ATCTTTAGACAGATTAATGCAAGGAGTGTAGTATTTCAATCTGACCGTGGCTTACATC 825
DB ATCTTTAGACAGATTAATGCAAGGAGTGTAGTATTTCAATCTGACCGTGGCTTACATC 1125
1066 ATCTTTAGACAGATTAATGCAAGGAGTGTAGTATTTCAATCTGACCGTGGCTTACATC 1125
DB ATCTTTAGACAGATTAATGCAAGGAGTGTAGTATTTCAATCTGACCGTGGCTTACATC 1125
826 TCAGAGCTGCTAAAGATTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 885
DB TCAGAGCTGCTAAAGATTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 885
1126 TCCTTTGAGGCAAAAGATTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1185
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RESULT 15

Query Match 12.5%; Score 218; DB 9; Length 4162;
Best Local Similarity 59.8%; Pred. No. 2.9e-43;
Matches 365; Conservative 0; Mismatches 245; Indels 0; Gaps 0;
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1817 CGGACGAGCGGCGAAGCTGCGGTGCAAGAGATCGGCAAGGAGGCTGCGGCCAGG 1876
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RESULT 14
US-09-938-842A-1063
Sequence 1063, Application US/09938842A
Patent No. US20020160378A1
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Krepis, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
FILE REFERENCE: SCRI1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 1063
LENGTH: 1800
TYPE: DNA

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US-09-938-842A-3678
; Sequence 3678, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPT300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
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; LENGTH: 718
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-3678

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Best Local Similarity 100.0%; Pred. No. 1.4e-37;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1615 CTAATTTCTAAGGATACAAAATATATCTGGCTTGTTTTGCTTTCCCTTTTATTTT 1674
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QY 1675 GTACATGAGCAACTTCTAAATTTTATCCCTCATATGATGATAATTTTGCCTTCATATAAAA 1734
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QY 1735 GTTTTGAATCC 1747
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Db 181 GTTTTGAATCC 193

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Search completed: March 26, 2003, 12:16:44
Job time : 513 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 25, 2003, 23:20:21 ; Search time 3002 seconds

(without alignments)
9424.889 Million cell updates/sec

Title: US-09-848-806-2

Perfect score: 1747

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Scoring table: IDENTIFY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743375 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estma:*

5: em_estov:*

6: em_estpl:*

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8: em_htc:*

9: gb_est1:*

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11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pln:*

21: em_gss_vrt:*

22: em_gss_fun:*

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25: em_gss_other:*

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27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	563.4	32.2	591	AV825282	AV825282 AV825282
3	523.6	30.0	2566	AY109374	AY109374 Zea mays
4	505.8	29.0	2298	AY109401	AY109401 Zea mays
5	503.8	28.8	507	AV558412	AV558412 AV558412
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DEFINITION Zea mays CL1905_1 mRNA sequence.
ACCESSION AY109473
VERSION AY109473.1 GI:21213206
KEYWORDS HTC.
SOURCE Zea mays.
ORGANISM Zea mays.
REFERENCE 1 (bases 1 to 2380)
AUTHORS Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S.,
Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
TITLE Maize Mapping Project/Dupont Consensus Sequences for Design of
JOURNAL Overgo Probes
REFERENCE 2 (bases 1 to 2380)
AUTHORS Unpublished (2002)
TITLE Direct Submission
JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of
Missouri, Columbia, MO 65211, USA
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AV790851 AV790851
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BQ506885 EST614300
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BQ967112 QHB28P17.
BI178918 EST519851
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BJ245960 BJ245960
BQ969859 QHB39L22.
BQ916638 QHB18118.
BQ970309 QHB41K23.
AV925405 AV925405
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BI074799 IPL_16.H1
AI894480 EST263923
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linear HTC 25-MAY-2002

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overgo addressing of BACs in conjunction with the Maize
Mapping Project."
BASE COUNT 478 a 560 c 507 g 468 t 367 others
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Best Local Similarity 60.7%; Pred. No. 1.5e-99;
Matches 859; Conservative 0; Mismatches 557; Indels 0; Gaps 0;
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Db 1969 CAATGAGAAACAGCTTGAATATCAGCATGAGGAGC 2004

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ACCESSION AV825282.1 GI:19867342
VERSION AV825282
KEYWORDS EST.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliopsida II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE 1 (bases 1 to 591)
AUTHORS Seki.M., Narusaka.M., Ishida.J., Kamiya.A., Satou.M., Nakajima.M.,
Oono.Y., Sakurai.T., Carninci.P., Kawai.J., Itoh.M., Ishii.Y.,
Arakawa.T., Shibata.K., Shinagawa.A., Muramatsu.M., Hayashizaki.Y.,
and Shinozaki.K.
TITLE Large scale analysis of Arabidopsis full-length cDNA (2002b)
JOURNAL Unpublished (2002)
COMMENT Contact: Motoaki Seki
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: mseki@rtc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998). cDNA cleaved with BamHI
and XhoI was ligated to modified Lambda FLU-1 vector (Carninci et
al., submitted for publication) digested with BamHI and SalI. This
clone is in a modified pBluescript vector. Please visit our web
site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further
details.

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DB 438 ATTTTAGTGAGCGTCAAGCTGTCAAGCTTATTAAAGACGATTTCTTGTTGTGAGGCTT 497
QY 488 GTCATCTCTTGGTGTATGATAGATCTCAAACTGAGATTTCTTGTGTTGATAGTC 547
DB 498 GACATCTCTTGGTGTATGATAGATCTCAAACTGAGATTTCTTGTGTTGATAGTC 557
QY 548 CTAAAGATCATGCTAAGCTTAAGGCTACCGATT 581
DB 558 CTAAAGATCATGCTAAGCTTAAGGCTACCGATT 591
RESULT 3
AY109374
LOCUS      AY109374      2566 bp      mRNA      linear      HTC 25-MAY-2002
DEFINITION Zea mays CUL146_1 mRNA sequence.
ACCESSION  AY109374
VERSION    AY109374.1 GI:21213078
KEYWORDS   HTC.
SOURCE     Zea mays.
ORGANISM   Zea mays.
REFERENCE  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 2566)
Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S.,
Arthur, L.W., Hanafe, M., Morgante, M. and Tingey, S.V.
TITLE      Maize Mapping Project/DuPont Consensus Sequences for Design of
Overgo Probes
JOURNAL    Unpublished (2002)
REFERENCE  2 (bases 1 to 2566)
AUTHORS    Coe, E.C.
TITLE      Direct Submission
JOURNAL    Submitted (25-APR-2002) Maize Mapping Project, University of
Missouri, Columbia, MO 65211, USA
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contigs to seed DuPont contigs; this resource was
assembled by DuPont as part of a collaboration for the
overgo addressing of BACs in conjunction with the Maize
Mapping Project"
BASE COUNT      440 a 680 c 777 g 420 t 249 others
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  Query Match      30.0%; Score 523.6; DB 11; Length 2566;
  Best Local Similarity 60.2%; Pred. No. 5.4e-86;
  Matches 799; Conservative 0; Mismatches 528; Indels 0; Gaps 0;
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DB 1298 GATACGGGCGAGAGGCGAGCTCTGGAGGCTGGCGCTTAATCATCTACATCTCTG 1357
QY 731 GTGTTCTCTCTTCTGGGCGAGAGCTAGTCTGAACTTTTACAGAGATTTTCAAGGGA 790
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overgo addressing of BACs in conjunction with the Maize
Mapping Project"

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Db	1206	GAGATAGATGTTGGAGCGCAGAGTGTTATTATTGTACATCTCTCAGTGGTGTGCGCTCCA	1265
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QY	862	GAAAGGAGCCCCAAGAAACGCATTTCTGCTCATGAAGCCCTTGTCTACCCCATGGATTGTC	921
Db	1386	ACAGGAGATCCAAAGAAAGAAAGACTGACTTCAGCTCAAGTTCTTCAACATTCATGGGCTCAGA	1445
QY	922	GATGAACAAGAGACACCGACAGACCCCTTTTGATCCAGCAGCTTATCTCGTCTTAAAGCAG	981

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Query Match	28.8%;	Score 503.8;	DB 10; Length 507;
Best Local Similarity	99.6%;	Pred. No. 3.6e-82;	
Matches 505;	Conservative	0; Mismatches	2; Indels 0; Gaps 0;
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Db	507	CCCTACACATGAACAAGATGGAGAGAGAGATCTCTGGTGCATTTTCGGTACTTTG	448
QY	1301	ACAAAGACGGAAGCGGTTATATCACCATCGATGAGCTTCAGTCAGCTGCACAGAGTTG	1360
Db	447	ACAAAGACGGAAGCGGTTATATCACCATCGATGAGCTTCAGTCAGCTGCACAGAGTTG	388
QY	1361	GTCTATGTGATACACCTCTGGACGACATGATCAAGGAGATGATCTTGACAATGACGGGA	1420
Db	387	GTCTATGTGATACACCTCTGGACGACATGATCAAGGAGATGATCTTGACAATGACGGGA	328
QY	1421	AGATCGATTTCTCGGAGTTTACAGCAATGATGAGAAAGGAGATGGAGTTGGGAGAGCA	1480
Db	327	AGATCGATTTCTCGGAGTTTACAGCAATGATGAGAAAGGAGATGGAGTTGGGAGAGCA	268
QY	1481	GAACCATGATGAAGAAGCTTGAACATTTCAACATTTCTCCACAATTTCTGTTTTTCTTTTAAATTCGT	1540
Db	267	GAACCATGATGAAGAAGCTTGAACATTTCAACATTTCTCCACAATTTCTGTTTTTCTTTTAAATTCGT	208
QY	1541	AATCTGATGACTGACTCATCTTCTCCACAATTTCTGTTTTTCTTTTAAATTCGT	1600
Db	207	AATCTGATGACTGACTCATCTTCTCCACAATTTCTGTTTTTCTTTTAAATTCGT	148
QY	1601	TTATATTTTGAATTTCTAATTTCTTAAGGATACAAAATATATATCTGGCTTGTGTTTTTTCCTTT	1660
Db	147	TTATATTTTGAATTTCTAATTTCTTAAGGATACAAAATATATATCTGGCTTGTGTTTTTTCCTTT	88
QY	1661	TCCTTTTATTTTGTACATGAGCAACTTCTTAAATTTTATCCCATATGATGATAATTTT	1720
Db	87	TCCTTTTATTTTGTACATGAGCAACTTCTTAAATTTTATCCCATATGATGATAATTTT	28
QY	1721	TGCTTCATATAAAGTTTTTGAATTC	1747
Db	27	TGCTTCATATAAAGTTTTTGAATTC	1
RESULT 6			
LOCUS	BG647837	835 bp	mRNA linear EST 24-APR-2001
DEFINITION	EST509456 HOGA Medicago truncatula cDNA clone phOGA-18E5 5' end,		
ACCESSION	BG647837		
VERSION	BG647837.1	GI:13782949	
KEYWORDS	EST.		
SOURCE	barrel medic.		
ORGANISM	Medicago truncatula		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
AUTHORS	Hahn, M.G., Ojanen-Reuhs, T., Samac, D., Town, C.D., Van Aken, S.,		
TITLE	Utterback, T., Cho, J. and Fraser, C.M.		
JOURNAL	ESTs from roots of Medicago truncatula treated with		
MEDLINE	oligogalacturonides of DP 6-20		
COMMENT	Unpublished (2001)		
	Contact: Michael G. Hahn		
	Complex Carbohydrate Research Center		
	University of Georgia		
	220 Riverbend Road, Athens, GA 30602-4712, USA		
	Tel: 706-542-4457		
	Fax: 706-542-4412		
	Email: hahn@ccrc.uga.edu		

1446	GAAGGTGGAGTGCATGTGATAAGCCATATCGACAGTGTCTTCTTCTAGAAATGAAGCAG	1505	
982	TTTTTCAATGAATAAGATTAGAAATGGCAATTCACGGGTAAATGCTGAGAGACTTTCA	1041	
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DEFINITION	Arabidopsis thaliana green siliques Columbia Arabidopsis thaliana cDNA clone SQ098b02F 3', mRNA sequence.		
ACCESSION	AV558412		
VERSION	AV558412.1	GI:8729838	
KEYWORDS	EST.		
SOURCE	thale cress.		
ORGANISM	Arabidopsis thaliana		
REFERENCE	Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.		
AUTHORS	A large scale analysis of cDNA in Arabidopsis thaliana: Generation		
TITLE	of 12,028 non-redundant expressed sequence tags from normalized and		
JOURNAL	size-selected cDNA libraries		
MEDLINE	DNA Res. 7, 175-180 (2000)		
COMMENT	20363093		
	Contact: Erika Asamizu		
	The First Laboratory for Plant Gene Research		
	Kazusa DNA Research Institute		
	Yana 1532-3, Kisarazu, Chiba 292-0812, Japan		
	Email: asamizu@kazusa.or.jp. URL: http://www.kazusa.or.jp/en/plant/.		
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BASE COUNT	179 a	104 c	80 g 144 t
ORIGIN			
Query Match	28.8%;	Score 503.8;	DB 10; Length 507;
Best Local Similarity	99.6%;	Pred. No. 3.6e-82;	
Matches 505;	Conservative	0; Mismatches	2; Indels 0; Gaps 0;
QY	1241	CCCTACACATGAACAAGATGGAGAGAGAGATCTCTGGTGCATTTTCGGACACTTTG	1300
Db	507	CCCTACACATGAACAAGATGGAGAGAGAGATCTCTGGTGCATTTTCGGTACTTTG	448
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QY	1361	GTCTATGTGATACACCTCTGGACGACATGATCAAGGAGATGATCTTGACAATGACGGGA	1420
Db	387	GTCTATGTGATACACCTCTGGACGACATGATCAAGGAGATGATCTTGACAATGACGGGA	328
QY	1421	AGATCGATTTCTCGGAGTTTACAGCAATGATGAGAAAGGAGATGGAGTTGGGAGAGCA	1480
Db	327	AGATCGATTTCTCGGAGTTTACAGCAATGATGAGAAAGGAGATGGAGTTGGGAGAGCA	268
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Db	267	GAACCATGATGAAGAAGCTTGAACATTTCAACATTTCTCCACAATTTCTGTTTTTCTTTTAAATTCGT	208
QY	1541	AATCTGATGACTGACTCATCTTCTCCACAATTTCTGTTTTTCTTTTAAATTCGT	1600
Db	207	AATCTGATGACTGACTCATCTTCTCCACAATTTCTGTTTTTCTTTTAAATTCGT	148
QY	1601	TTATATTTTGAATTTCTAATTTCTTAAGGATACAAAATATATATCTGGCTTGTGTTTTTTCCTTT	1660
Db	147	TTATATTTTGAATTTCTAATTTCTTAAGGATACAAAATATATATCTGGCTTGTGTTTTTTCCTTT	88
QY	1661	TCCTTTTATTTTGTACATGAGCAACTTCTTAAATTTTATCCCATATGATGATAATTTT	1720
Db	87	TCCTTTTATTTTGTACATGAGCAACTTCTTAAATTTTATCCCATATGATGATAATTTT	28
QY	1721	TGCTTCATATAAAGTTTTTGAATTC	1747
Db	27	TGCTTCATATAAAGTTTTTGAATTC	1
RESULT 6			
LOCUS	BG647837	835 bp	mRNA linear EST 24-APR-2001
DEFINITION	EST509456 HOGA Medicago truncatula cDNA clone phOGA-18E5 5' end,		
ACCESSION	BG647837		
VERSION	BG647837.1	GI:13782949	
KEYWORDS	EST.		
SOURCE	barrel medic.		
ORGANISM	Medicago truncatula		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
AUTHORS	Hahn, M.G., Ojanen-Reuhs, T., Samac, D., Town, C.D., Van Aken, S.,		
TITLE	Utterback, T., Cho, J. and Fraser, C.M.		
JOURNAL	ESTs from roots of Medicago truncatula treated with		
MEDLINE	oligogalacturonides of DP 6-20		
COMMENT	Unpublished (2001)		
	Contact: Michael G. Hahn		
	Complex Carbohydrate Research Center		
	University of Georgia		
	220 Riverbend Road, Athens, GA 30602-4712, USA		
	Tel: 706-542-4457		
	Fax: 706-542-4412		
	Email: hahn@ccrc.uga.edu		

G391443e TIGR sequence name: MTMCE27TK More information is available at: www.medicago.org
Seq primer: skmod (CTA GAA CTA gtg gat CC).

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BASE COUNT 230 a 137 c 210 g 258 t
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Query Match 27.7%; Score 484; DB 12; Length 835;
Best Local Similarity 75.2%; Pred. No. 1.3e-78;
Matches 629; Conservative 0; Mismatches 205; Indels 2; Gaps 2;

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DB 122 GAGAAATTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 181
QY 586 TTGCTCTCTCTATAGCCAGGACATATTTATATGACGTAGTGTGAAGTCTGCTACTAT 645
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QY 706 GTTATCCTCTACATTTTACTCAGCGGTGTTCTCCTCCTCTGCGGACAGACTGAGTCTGGA 765
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DB 422 TCAGACAGTGCACAGGATCTAATTCGAAAAATGCTTATAGGAACCCCAAAACAGATT 481
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QY 1066 GAAATTTTCAAGATGATAGACACAGACAGCGGAAGATTAATTTTGAAGAGCTCAAA 1125
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RESULT 7

AY109463/c 1628 bp mRNA linear HTC 25-MAY-2002
LOCUS Zea mays CL10776.2 mRNA sequence.
DEFINITION Zea mays
ACCESSION AY109463
VERSION AY109463.1 GI:21213192
KEYWORDS HTC
SOURCE Zea mays.
ORGANISM Zea mays

REFERENCE 1 (bases 1 to 1628)
AUTHORS Hainey C.F., Dolan M., Miao G.H., Vogel J.M., Whitsitt, M.S., Arthur L.W., Hanafey M., Morgante M. and Tingey S.V.
TITLE Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes
REFERENCE 2 (bases 1 to 1628)
AUTHORS Coe E.C.

Direct Submission
Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA
Location/Qualifiers

FEATURES

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/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"

BASE COUNT 393 a 408 c 350 g 424 t 53 others
ORIGIN

Query Match 27.5%; Score 480.6; DB 11; Length 1628;
Best Local Similarity 60.0%; Pred. No. 4.3e-78;
Matches 775; Conservative 0; Mismatches 514; Indels 3; Gaps 1;

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QY 229 AAATCGATCCCGAAGCGAAAGCTGTGTGCGGAGGATTACGAAATGATGATGGCGTGAG 288
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DEFINITION	BG887873 EST513724 cSTD Solanum tuberosum cDNA clone cSTD7P13 5' sequence, mrna sequence.
ACCESSION	BG887873
VERSION	BG887873.1 GI:14264959
KEYWORDS	EST.
SOURCE	potato. Solanum tuberosum
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum. 1 (bases 1 to 814)
REFERENCE	van der Hoeven,R.J., Bezzerides,J., Ewing,E., Cho,J., Chiemingo,A., Bougrit,O., Buell,C.R., Roming,C., Tanksley,S. and Baker,B. Generations of ESTs from dormant potato tubers Unpublished (2001)
AUTHORS	Contact: Cathy Renning
TITLE	
JOURNAL	
COMMENT	

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FEATURES
source
seq primer: wlsf-R.
Location/Qualifiers
1. .814
/organism="Solanum tuberosum"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="cSTD7p13"
/clone_lib="cSTD"
/tissue_type="dormant tuber"
/dev_stage="one month post-harvest"
/lab_host="SOLR"
/note="Vector: pbluescript SK(-); Site1: EcoRI; Site 2:
XhoI; This library targets genes expressed in dormant
tubers. This library was made from sections of dormant
tubers, avoiding the buds and epidermis. Tubers were stored
for one month post-harvest at 40C. The tuber was peeled,
well away from the surface. Then it was chopped into 1-2
mm cubes and immediately frozen in liquid nitrogen. This
library is noted as P4 in Tanksley lab notebooks."
242 a 146 c 191 g 235 t
BASE COUNT

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BASE COUNT      242 a   146 c   191 g   235 t
ORIGIN
Query Match          26.7% ; Score 466.8; DB 12; Length 814;
Best Local Similarity 73.3%; Pred No. 1.8e-75;
Matches 597; Conservative 0; Mismatches 217; Indels 0; Gaps 0;

QY 438 GGGTGAAGCTGTCAAGCTATTAAACGATTCCTTGCGTTGTGTAGGCTGTGCATCTCT 497
DB 1 GAGAAAAGCTGCACAATTTGATGAAACTATTGTCAAAGTGTGGAGGCTGTGCATCTCT 60
QY 498 TGGCTTTATGCATAGAGATCTCAAACCTCAGAATTTCTTTGTGATGTCTCTAAGATGA 557
DB 61 TGGGTTTAAGCATAGAGATCTCAAACCTCAGAATTTCTTTGTGATGTCTCTAAGATGA 120
QY 558 TGCTAAGCTTTAAGGCTACCGATTTTTGGGTTTGTCTCTCTATAAGCCAGGACAAATATT 617
DB 121 TGCTAAGCTTTAAGGCTACTGATTTTGGTCTCTCTATTTCTATAAGCCAGGSCAGTATT 180
QY 618 ATATGACGTAGTTGGAAGTCCGTACTATGTTGCACCAGAGGTGCTTAAGAAATGTTATGG 677
DB 181 CTCAGATGTTGTGGAAGTCCATATATTGTTGCTCCTCAAGTGTGTCACAAATCTATGG 240
QY 678 ACCTGAATAGATGTGTGAGTGTGGTGTGTTATCCTCTACATTTTACTCAGGGGTGTGCC 737
DB 241 GCCTGAAATAGACGCTGTGAGTGTGGASTCATCCTTTATATCTTGTATGTGGGGTGTCC 300
QY 738 TCCCTTCTGGGCAGAGACTGAGTCTGGAACTPTTAGACAGATATTGCAAGGGAAGTTAGA 797
DB 301 TCCCTTCTGGGCTGAGACAGACAATGGTATCTTCAACACAGATATTAAAGGNAAGATAGA 360
QY 798 TTTCAAATCTGACCGGTGGCCCTACTATCTCAGAAGCTGCTAAGAGATTTTGATCTATAAAT 857

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Db 361 CTTTGAATCAGAACCTTGGCCCTCAGATTCCTGATAGTGCAGAAAGATTTGGTAAGAAGAT 420
QY 858 GGTGAAAGAGGCCCAAGAAAGCAATTTCTGCTCATGAAGCCTTGTGTACCCCATGGAT 917
Db 421 GCTCACCAGGGATCCTAGAGCAGCATTAACCGCGCATCAAGTTCATGTATCCTCTGGAT 480
QY 918 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 977
Db 481 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
QY 978 GCAGTTTCTCAAAATGAATTAAGAAATTAAGAAATTAAGAAATTAAGAAATTAAGAAATTAAG 1037
Db 541 GCAGTTTCTATGATATGAACAACTTAAAGAGTGGCTTTACGAGTCAATAGCAGAAAGGCT 600
QY 1038 TTCAGAGGAAGAAATTTGGAGGCTTGAAGAAATTTGAAGAAATTTGAAGAAATTTGAAGAAATTTGA 1097
Db 601 TTCAGAGGAAGAAATTTGGAGGCTTGAAGAAATTTGAAGAAATTTGAAGAAATTTGAAGAAATTTGA 660
QY 1098 CGGAAGCATTTTGAAGAGCTCAAGCGGCTTGAAGAGCTCAAGCGGCTTGAAGAGCTCAAGCGGCT 1157
Db 661 TGAACAATCACAATGAGAACTTAAACATGATGTTTGAAGAGCTCAAGCGGCTTGAAGAGCTCAAG 720
QY 1158 GGAATCAGAAATCAAGTCTCTCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1217
Db 721 AGAGTCGAAATCAAGGCTTGTATGAGCGGCTGACTTTGACAACACGCGCACTATCGAC 780
QY 1218 CTACGGAGATTTCTAGCAGCAACCTTACACATG 1251
Db 781 TATGGTGAATTCATCGCTGCAACATTTGCATTTG 814

RESULT 9
B28263/c
LOCUS
DEFINITION T8A20T7B TAMU Arabidopsis thaliana genomic clone T8A20, DNA
sequence.
ACCESSION B28263
VERSION B28263.1 GI:2514229
KEYWORDS GSS.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 493)
Rounsley,S.D., Kelley,J.M., Field,C.E., Craven,M.B., Adams,M.D. and
Venter,J.C.
Use of a BAC End Sequence Database To Identify Minimal Overlaps for
Arabidopsis Genomic Sequencing
Unpublished (1997)
Other_GSSs: T8A20TR
Contact: Steve Rounsley
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: rounsley@tigr.org
Seq primer: M13-21
Class: BAC ends
High quality sequence stop: 493.
Location/Qualifiers
1. 493
/organism="Arabidopsis thaliana"
/strain="Columbia"
/db_xref="taxon:3702"
/clone="T8A20"
/clone_lib="TAMU"
/sex="hermaphrodite"
/note="Vector: BeLoBACII; Site_1: HindIII; Site_2: HindIII
; Produced by Rod Wing"

BASE COUNT 126 a 110 c 95 g 162 t

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 2.4e-70;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 18 TTTCTTCTTCTTCAAAATCGAGATCGAAGAGAACCAACAAAAACCAAAAAATCGAGACGAA 77
Db 440 TTTCTTCTTCTTCAAAATCGAGATCGAAGAGAACCAACAAAAACCAAAAAATCGAGACGAA 381
QY 78 GCCAAACCCCTAGACGCTTCAACACACAGTTCTTACCATATCAACACACACGATTAGAGA 137
Db 380 GCCAAACCCCTAGACGCTTCAACACACAGTTCTTACCATATCAACACACACGATTAGAGA 321
QY 138 TCATTACCTTCTGGGAAAAAGCTAGGCCAAGGCCAAATTTGGAACAACCTATCTCTGAC 197
Db 320 TCATTACCTTCTGGGAAAAAGCTAGGCCAAGGCCAAATTTGGAACAACCTATCTCTGAC 261
QY 198 AGAAGAAATCAACCTCGCTAAATTTACGCTTGAATTCGATCCCGAAGCGAAAGCTCGTGT 257
Db 260 AGAAGAAATCAACCTCGCTAAATTTACGCTTGAATTCGATCCCGAAGCGAAAGCTCGTGT 201
QY 258 TCGCGAGGATTCAGAAATGATGATGCGCTGAGATTCAGATTCAGATTCATCTCTGACGA 317
Db 200 TCGCGAGGATTCAGAAATGATGATGCGCTGAGATTCAGATTCAGATTCATCTCTGACGA 141
QY 318 TCCAAATGTTTGTAGATCAAGGAGCTTATGAGATTCGATTCGATTCGATTCGATTCGAT 377
Db 140 TCCAAATGTTTGTAGATCAAGGAGCTTATGAGATTCGATTCGATTCGATTCGATTCGAT 81
QY 378 GGAGTTTGTGAAGTGGTGGCTTTTGTGATCGGATTTTGTGATCGGATTTTGTGATCGGATTTTGT 437
Db 80 GGAGTTTGTGAAGTGGTGGCTTTTGTGATCGGATTTTGTGATCGGATTTTGTGATCGGATTTTGT 21
QY 438 GCGTGAAGCTGTCAAGCTT 456
Db 20 GCGTGAAGCTGTCAAGCTT 2

RESULT 10
B11596/c
LOCUS
DEFINITION T8A20-T7 TAMU Arabidopsis thaliana genomic clone T8A20, DNA
sequence.
ACCESSION B11596
VERSION B11596.1 GI:2092717
KEYWORDS GSS.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 1087)
Feng,J., Dewar,K., Buehler,E., Kim,C., Li,Y., Shinn,P., Sun,H. and
Ecker,J.
BAC End Sequences at ATGC
Unpublished (1997)
Contact: Ecker J.
Arabidopsis Thaliana Genome Center
University of Pennsylvania
Dept. of Biology, University of Pennsylvania, Philadelphia, PA
19104
Tel: 215-898-9384
Fax: 215-898-8780
Email: jockey@atgenome.bio.upenn.edu
Seq primer: T7
Class: BAC ends
High quality sequence start: 93
High quality sequence stop: 873.
Location/Qualifiers
1. 1087
/organism="Arabidopsis thaliana"
/strain="Columbia"

FEATURES
source
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/db_xref="taxon:3702"
/clone="T8A20"
/clone_lib="TAMU"
/sex="hermaphrodite"
/note="Vector: BeLoBACII; Site_1: HindIII; Site_2: HindIII
; Produced by Rod Wing"
BASE COUNT 308 a 206 c 178 g 392 t 3 others
ORIGIN
Query Match 25.1%; Score 437.8; DB 17; Length 1087;
Best Local Similarity 98.4%; Pred. No. 3.1e-70;
Matches 442; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 8 GTACATATCTCTCTCTCTCTCAATCGAGATCGAGAGACCAACCAACCAAAA 67
DB 495 GTTATTCATCTCTCTCTCTCTCAATCGAGATCGAGAGACCAACCAACCAAAA 436

QY 68 TGGAGACGAAGCAACCCCTAGACGTCCTTCAACACACAGCTTACCATATCAACACCAAC 127
DB 435 TGGAGACGAAGCAACCCCTAGACGTCCTTCAACACACAGCTTACCATATCAACACCAAC 376

QY 128 GATTAGAGATCATTACCTTCTCGGAAAAAAGCTAGCCCAAGGCCAATTTGGAACAACCT 187
DB 375 GATTAGAGATCATTACCTTCTCGGAAAAAAGCTAGCCCAAGGCCAATTTGGAACAACCT 316

QY 188 ATCTCTGCACAGAGAATCAACCTCCGCTAATTAACGCTGCAAAATCGATCCGGAAGCGAA 247
DB 315 ATCTCTGCACAGAGAATCAACCTCCGCTAATTAACGCTGCAAAATCGATCCGGAAGCGAA 256

QY 248 AGCTCGTGTGTCGCGAGGATACGAAGATGTATGGCGTGAGATTCAGATCATCATCATC 307
DB 255 AGCTCGTGTGTCGCGAGGATACGAAGATGTATGGCGTGAGATTCAGATCATCATCATC 196

QY 308 TCCTGAGCATCAAAATGTTTGTAGGATCAAGGGACTTATGAAGATTCGGTGTGTTGTTTC 367
DB 195 TCCTGAGCATCAAAATGTTTGTAGGATCAAGGGACTTATGAAGATTCGGTGTGTTGTTTC 136

QY 368 ATATTGTTAGGAGTTGTGAGGTGCTGAGCTTTTGTGCGGATTTGTTCTTAAAGGTC 427
DB 135 ATATTGTTAGGAGTTGTGAGGTGCTGAGCTTTTGTGCGGATTTGTTCTTAAAGGTC 76

QY 428 ATTTAGTACGCTGAGCTGTCAAGCTT 456
DB 75 ATTTAGTACGCTGAGCTGTCAAGCAT 47

RESULT 11
AI994248
LOCUS 528 bp mRNA linear EST 08-SEP-1999
DEFINITION 701501524 A. thaliana, Ohio State clone set Arabidopsis thaliana
CDNA clone 701501524, mRNA sequence.
ACCESSION AI994248
VERSION AI994248.1 GI:5841153
KEYWORDS EST.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1 (bases 1 to 528)
Chen, J., Moniyama, M., Chan, E., Mooney, M., Carroon, B., Gilliland, D.,
Wang, X., Hillman, J., Guebler, K., Kim, C., Doyle, M., Brzoska, P.,
Gorgone, C., Burns, D., Griffin, J., Mouanoutoua, M., Nguyen, D., Tan, R.,
Rose, M., Warren, B., Ton, B., Kastury, K., Borillo, C., Carpio, T.,
Policky, J., Suzuki, G., Argentine, C., Shah, S., Nobriga, A., Murry, L.,
Turner, C., Krikorian, S., Elder, L. and Hanson, D.
Arabidopsis thaliana Gene Expression MicroArray
Unpublished (1999)
Contact: David Smoller, Ph.D.
Genome Systems, Inc., a wholly owned subsidiary of Incyte
Pharmaceuticals, Inc.
4633 World Parkway Circle, St. Louis, MO 63134, USA
Tel: 877-577-2733

```

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Fax: 314-427-3324
Email: service@genomesystems.com.
Location/Qualifiers
1. 528
/organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
/clone="701501524"
/clone_lib="A. thaliana, Ohio State clone set"
/note="CDNA library was made from selected clones from the
Arabidopsis thaliana Ohio State clone set."
BASE COUNT 160 a 100 c 136 g 132 t
ORIGIN
Query Match 24.3%; Score 424.8; DB 9; Length 528;
Best Local Similarity 92.3%; Pred. No. 9.1e-68;
Matches 480; Conservative 0; Mismatches 37; Indels 3; Gaps 3;

QY 925 GAACAGCAGCAGCAGCAGCAGCCTCTTGATCCAGCAGCTTATCTCGTCTAAGCAGTTT 984
DB 6 GAACAGCAGCAGCAGCAGCAGCCTCTTGATCCAGCAGCTTATCTCGTCTAAGCAGTTT 65

QY 985 TCTCAATGAATTAAGATTAAAGAAATGGCATTACGGTAAATGCTGAGAGACTTTCAGAG 1044
DB 66 TCTCAATGAATTAAGATTAAAGAAATGGCATTACGGTAAATGCTGAGAGACTTTCAGAG 125

QY 1045 GAAGAAATTTGGAGTCTGTAAGGAATTTGTTCAAGATGATAGACACAGACGCGGAACG 1104
DB 126 GAAGAAATTTGGAGTCTGTAAGGAATTTGTTCAAGATGATAGACACAGACGCGGAACG 185

QY 1105 ATTACTTTTGAAGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1163
DB 186 ATTACTTTTGAAGGAGCTCAAGCGGTTTGAAGAGAGTCGGGTCTTAACTGGTGAATC 245

QY 1164 AGAATCAAGTCTCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1223
DB 246 AGAATCAAGTCTCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 305

QY 1224 AGAATCCTAGCAGCAACCTTACACATGAACAAGATGGAGAGAGAGAGATTCCTGGTGC 1283
DB 306 AGAATCCTAGCAGCAACCTTACACATGAACAAGATGGAGAGAGAGAGATTCCTGGTGC 365

QY 1284 TGCATTTTCGACCTTTCGACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1342
DB 366 TGCATTTTCGACCTTTCGACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 424

QY 1343 CAGCTTCACAGAGTTTGGTCTATGATACACCTCTGGAGCAGATCATCAAGGAGATTG 1402
DB 425 CAGCTTCACAGAGTTTGGTCTATGATACACCTCTGGAGCAGATCATCAAGGAGATTG 484

QY 1403 ATCTTGACAATGACGGGAAGATGATTCCTCGGAGTTTAC 1442
DB 485 GTCTTTACAATGACGGGAAGATGATTCCTCGGAGTTTTC 524

RESULT 12
BG596613 742 bp mRNA linear EST 12-APR-2001
LOCUS BG596613
DEFINITION EST459291 cSTS Solanum tuberosum cDNA clone cSTS15M13 5' sequence,
mRNA sequence.
ACCESSION BG596613
VERSION BG596613.1 GI:13614753
KEYWORDS EST.
SOURCE potato.
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
1 (bases 1 to 742)
van der Hoeven, R., Bezzerides, J., Sun, H., Cho, J., Chiemingo, A.,
Bougri, O., Buel, C., Ronning, C., Tanksley, S. and Baker, B.
Generations of ESTs from sprouting potato eyes
Unpublished (2000)
Contact: Cathy Ronning

```


The Institute for Genomic Research
For clone info: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com
Seq primer: M13F-R.

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FEATURES
Source
1..742
/organism="Solanum tuberosum"
/cultivar="kennebec"
/db_xref="taxon:4113"
/clone="cSTS15M13"
/clone_lib="cSTS"
/tissue_type="sprouting eyes from tubers"
/dev_stage="12-14 weeks post harvest"
/lab_host="SOLR"
/notes="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; Various sizes of sprouting eyes (2mm to 15mm) were
taken from tubers. The tubers were incubated at 26C in the
dark for 2-3 weeks prior to sprouting. The eyes were
frozen in liquid nitrogen immediately upon removal from
tubers."
BASE COUNT 214 a 128 c 181 g 219 t
ORIGIN
Query Match 23.9%; Score 418; DB 12; Length 742;
Best Local Similarity 74.1%; Pred. No. 1.4e-66;
Matches 529; Conservative 0; Mismatches 185; Indels 0; Gaps 0;
QY 106 GTTCTACCATATCAACACACACAGATTAAGAGATCATTTACCTTCTGGGAAAAAGCTAGGC 165
Db 22 GTTCTCCCTTACAGACTGAAGACCTTCAGCAGCTTTTACAGATATAGGAAAAAATTAGG 81
QY 166 CAAGGCCAAATTGGAAACAACCTATCTCTGCACAGAGAAATCAACCTCCGCTAATTAGCC 225
Db 82 CAGGCCAAATTGGAAACCACCCATTTATGTACAGAAAAATCAACTGCTACTCTTTATGCT 141
QY 226 TGCAAATCGATCCGAGAGGAAGCTCGTGTGCGGAGGATTACGAGATGTATGCGCT 285
Db 142 TGCAGACTATACCAAGAGAGAGTTGATTGTGAAGAGGATTATGAGGATGTTGGAGG 201
QY 286 GAGATTCAGATCATGATCATCTCTGAGCATCCAAATGTTGTAGGATCAAGAGGACT 345
Db 202 GAGATTCAGATATGACCAATTTATCTGACACCCAAATGTTGTCAGATTAAGGGTACT 261
QY 346 TATGAAGATTCGGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 405
Db 262 TATGAAGATACCTTATATGTCACATAGTTATGAGCTTTGTTGTTGTTGTTGTTGTTGTT 321
QY 406 GATCGGATGTTCTAAGGTCATTTTAGTGAGCGTGAAGCTGTCAAGCTTATTAAGACG 465
Db 322 GATAGGATCGTTGAAAGGGACATTCAGTGAAGGGAGAGCTGCGAAGCTTATTAAGACT 381
QY 466 ATTCTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 525
Db 382 ATTCTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 441
QY 526 GAGAAATCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 585
Db 442 GAGAAATCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 501
QY 586 TTGTCCTGTTCTATAGCCAGGACATATTTATGACGTAGTGTGAGTCCTGCTACTAT 645
Db 502 CTCCTCGTTTCTACCGCCAGGGAATGTTTCCGATGTTGTTGAGTCCCTTACTAT 561
QY 646 GTTGCCAGAGGCTGCTAAAGAAATGTTATGACCTGAAATAGATGTGTGAGTGTGCTGGT 705
Db 562 GTTGACCTGAGTTTACGCAAGCATTTATGACCTGATCTGATGTATGATGAGCGCAGGA 621
QY 706 GTTATPCTCTACATTTTACTCAGCGGTGTTCTCCCTCTCGGCGAGACTGAGTGTGGA 765
Db 622 GTTATTTGTACATATTAATAGTGGGCTTCCACCTTTTGGGAGAACTGAGATGGA 681
QY 766 ATCTTTACAGATATTCAGAGGAAGTGTAGATTTCAATCTGACCCGTGGCCT 819

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Db 682 ATATCCGCCAGATATTGCAAGCAAAATAGATTGTAATCTGACCATGGCT 735
RESULT 13
LOCUS BM779035
DEFINITION BM779035 813 bp mRNA linear EST 04-MAR-2002
sequence. EST589610 KV2 Medicago truncatula cDNA clone pkV2-22111, mRNA
ACCESSION BM779035
VERSION BM779035.1 GI:19108729
KEYWORDS EST.
SOURCE barrel medic.
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabcaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE 1 (bases 1 to 813)
AUTHORS VandenBosch,K., Endre,G., Hur,J., Beremand,P., Town,C.D., Van Aken
,S., Utterback,T., Cheung,F., Tsai,J. and Fraser,C.M.
TITLE ESTs from roots of Medicago truncatula 48 hr after inoculation with
Sinorhizobium meliloti
JOURNAL Unpublished (2002)
COMMENT Contact: VandenBosch K
Department of Plant Biology
University of Minnesota
220 Biosci Center, 1445 Gortner Ave, St. Paul, MN 55108, USA
Tel: 612 624 2755
Fax: 612 625 1738
Email: kvandenb@cbs.umn.edu
TIGR sequence name: MTABK54TK More information is available at:
www.medicago.org
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
FEATURES
Location/Qualifiers
1..813
/organism="Medicago truncatula"
/cultivar="genotype A17"
/db_xref="taxon:3880"
/clone="pkV2-22111"
/clone_lib="KV2"
/tissue_type="Seedling roots"
/dev_stage="2 days post-inoculation with Sinorhizobium
meliloti"
/lab_host="E. coli strain SOLR"
/notes="Vector: pBluescript SK -; Site_1: EcoRI; Site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA. The
cDNA was directionally ligated into the Unizap XR vector
from Stratagene and packaged using Gigapack III Gold
packaging extracts. Plasmids containing cDNA inserts
were excised from the recombinant lambda-zap phage using
Ex-assist helper phage and propagated in SOLR cells."
BASE COUNT 229 a 151 c 188 g 245 t
ORIGIN
Query Match 23.0%; Score 402.4; DB 14; Length 813;
Best Local Similarity 74.0%; Pred. No. 9.7e-64;
Matches 536; Conservative 0; Mismatches 186; Indels 2; Gaps 2;
QY 106 GTTCTACCATATCAACACACAGATTAAGAGATCATTTACCTTCTGGGAAAAAGCTAGGC 165
Db 91 GTTCTCCCTTATGTTAACTGAAATCTTCGTGAAGTTTACACCTTAGCAGAAACTGGGT 150
QY 166 CAAGGCCAAATTGGAAACAACCTATCTCTGCACAGAGAAATCAACCTCCGCTAATTAGGCC 225
Db 151 CAAGGTCAUATTGGGATCATATCACTGTCATACACAACCTCAACGGGTAGAACCTAGCT 210
QY 226 TGCAAATCGATCCGAGCGAAGCTCGTGTGCGGAGGATTACGAGATGTATGCGCT 285
Db 211 TGCAAATCAATCTCAAGAGAGAGCTTTTATGCAAGAGGATTTATGATGATGTTGAGA 270
QY 286 GAGATTCAGATCATGATCTCTCTGAGCATCCAATGTTGTAGGATCAAGAGGACT 345
Db 271 GAGATTCAGATTAATGACCATTTGTCGAAATCCAATGTTGTGAGATCCATGGA 330

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BQ865474
LOCUS
DEFINITION QG5A16.yg.ab1 QG-ABCD1 lettuce salinas Lactuca sativa cDNA clone
QGC5A16, mRNA sequence.
ACCESSION BQ865474
VERSION BQ865474.1 GI:22250939
KEYWORDS EST.
SOURCE Lactuca sativa.
ORGANISM Lactuca sativa.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
Lactuca.
1 (bases 1 to 751)
Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,
Lin,H., van Damme,M., Lavelle,D., Chevallier,P., Ziegler,J., Ellison
,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z.,
Church,S., Jackson,L. and Bradford,K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
http://compenomics.ucdavis.edu/
Unpublished (2002)
Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@ucdavis.edu [michelmore@vegmail.ucdavis.edu]
belongs to contig QG_CA.Contig3691, see http://cgpdb.ucdavis.edu/
for details.
Plate: QGC5 row: A column: 16.
FEATURES
Location/Qualifiers
1..751
/organism="Lactuca sativa"
/cultivar="Salinas"
/db_xref="taxon:4236"
/clone="QG5A16"
/lab_host="QG-ABCD1 lettuce salinas"
/lab_host="E.coli"
/note="Vector: pBRCNDSFIAB; The library was constructed
from 10 different sources of RNA from a single genotype.
Separate cDNAs were generated using primers that
incorporated unique 5' and 3' tags to distinguish each
source of RNA. cDNAs were then pooled, size-fractionated,
directionally cloned into a custom medium-copy vector and
transformations made with four size classes to minimize
size bias. Details of each source of RNA and library
construction can be obtained at http://cgpdb.ucdavis.edu/
TAG.LIB=QG-ABCD1 lettuce salinas
TAG.TISSUE=chemical induction
TAG_SEQ=TGATGCGGG"
BASE COUNT 218 a 117 c 180 g 236 t
ORIGIN
Query Match 22.3%; Score 388.8; DB 14; Length 751;
Best Local Similarity 70.9%; Pred. No. 3e-61;
Matches 530; Conservative 0; Mismatches 217; Indels 1; Gaps 1;
QY 287 AGATTCAGATCAATGATCTCTCTGAGCATCCCAATGTTGTAGGATCAAGGACCT 346
DB 1 AGATTCAGATCAATGATCTCTCTGAGCATCCCAATGTTGTAGGATCAAGGACCT 60
QY 347 ATGAGATTCGTTGAGGCTGATGTTGTTGAGGCTGTTGTTGAGGCTGTTG 406
DB 61 ATGAGATTCGTTGAGGCTGATGTTGTTGAGGCTGTTGTTGAGGCTGTTG 120
QY 407 ATCGGATGTTTCTAAAGGTCATTTAGTGAGCGGTGAAGCTGTCAAGCTTATTAAAGCGA 466
DB 121 ATAGGATTTCAAGAGGACATACACTGAAAAAAGCAGCTGAGCTTACAAAGCGA 180
QY 467 TTCTTGGTGTGTGAGGCTGTGCTCTCTGTTGTTGTTGTTGTTGTTGTTGTTG 526
DB 181 TTGTTGGGTTGTGGAGACTGTGCTCTCTGTTGTTGTTGTTGTTGTTGTTGTTG 240

QY 527 AGATTTCTTTGTTGATAGTCCTAAAGATGATGCTAAGCTTAAAGGCTAACGGAATTTGGTT 586
DB 241 AAAATTTCTTTGCTTTGTTGATGAAGAAGAAGATTCGCTTCTCAAAACTATTGATTTGGAT 300
QY 587 TGTCTGTCTTCTATAGCCAGGACAATATTATATGACGTAGTTGGAGTCCGCTACTATG 646
DB 301 TATCGGTTTCTTCAAAACCAGGTGAATCAATTAATGATGTGGTTGGAAGCCCATATTATG 360
QY 647 TTGCACACAGAGGCTCTAAAGAAATGTTATGACCTGAATAGATGTTGAGTCTCTGTTG 706
DB 361 TTGCACACAGAGGTTTGGAGAAAACGTTATGCGCTGAAGCAGAGGTTTGGAGTCTCTGGG 420
QY 707 TTATCTCTTACATTTTACTCAGCGGTGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 766
DB 421 TTATGTTTATCTTATTAAGTGTGTACCTCCATTTTGGGCTGAAACGAGCAAGGAA 480
QY 767 TCTTTAGACAGATATTGCAAGGGAAGTTAGATTTCAAATCTGACCCGCTGGCTACTATCT 826
DB 481 TATTTGAACAAGTCTCTCAAGGCGATCTTGATTTCTCTCTCTCTCTCTCTCTCTCTCTCT 540
QY 827 CAGAGCTGTCTAAAGATTGATCTATAAATGCTCGAAAGGAGGCCCAAGAAAGCGCATTT 886
DB 541 CTGAGATGCAAAAGATCTTGTAAAGGCAATGCTTATTCGAGACCTTAAAGAGACGATTAA 600
QY 887 CTGCTCATGAAGCCCTTGTGTCAACCATGGATTGCGATGAACAAGCAGCACCACACAAGC 946
DB 601 CTGCACATGAAGTTTATGTCTCATCTTGGGTTCAAGTTGATGGGCTGGCTCCAGACAAGC 660
QY 947 CTCTGTATCCAGCAGCTCTTATCTCGTCTAAAGCAGTTTCTCAATGAATGAATTAAGA 1006
DB 661 CTCTGAGCTCTGAGTCTCTAAGTAGAATGAA-CAATTTTTCAGCCCATGAATGAATGA 719
QY 1007 AAATGGCATTTACGGGTAATTTGCTGAGAG 1034
DB 720 AAATGGCTTTGAGGGTTTATAGCTGAGAG 747

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